GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

- protein search, using sw model OM protein

Run on:

April 23, 2003, 11:01:50 ; Search time 39 Seconds (Without alignments) (Without alignments) (217:477 Million Cell updates/sec

US-10-004-551-6 3400 MSAAMSIFLIGYKIGLFLQ.....SSSNRSYROSGIPDSDHSHS 649 Perfect score: Sequence:

Title:

908470 seqs, 133250620 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Database :

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Pred. No. 1s the number of results predicted by chance to have a core greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS2/gcgdxta/geneseq/geneseqp-emb1/AA2000.DAT:*/SIDS2/gcgdxta/geneseq/geneseag-emb1/AA2001.DAT:*/SIDS2/gcgdata/geneseq/geneseag-emb1/AA2002.DAT:*

·embl/Aa1999.DAT:*

/SIDS2/qcgdata/geneseq/genesegp

SUPPRIES

	- 51									
Description	Human PRO polypept	Human PRO1865. Ho	Human PRO3 protein	Human anglogenesis	Human PRO1865 prot	Human protein sequ	Human protein SBO	Human polypeptide,	Murine skin cell p	Skin cell protein,
а	AAU29215	AAB87591	AAB70533			AAB93758			AAY76050	AAB55989
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	ABB72189 AAU19626	553	623	9.96	3284	72 2

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ALIGNMENTS

AAU29215 standard; Protein; 649 AA. 18-DEC-2001 (first entry)

RESULT 1

PRO polyperficide meanal; tramour; concorr; human; orticle; horse; sheep; dog only pig; ort; pig; oper; rabbir; tramour; necrocis factor alpha; TRF-alpha; blood; denderocyte ent.; edi. proliferation; od. differation; diffe Juman PRO polypeptide sequence #192.

W0200168848-A2. Homo sapiens.

20-SEP-2001

20000S-189328P. 20000O-US06884. 2000US-190828P. 2000US-191007P. 2000US-191048P. 28-FEB-2001; 2001WO-US06520 2000WO-US05841 2000US-187202P 20000S-186968P. 20000S-189320P. 2006WO-US05601 02-NAR-2000; 2 03-NAR-2000; 2 06-NAR-2000; 2 14-NAR-2000; 2 115-NAR-2000; 2 21-NAR-2000; 2 21-NAR-2000; 2 01-MAR-2000;

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presence of tumours, such as prostate and breast tumours, in mammals and 
to screen for modulators of the compounds
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ith V, Watanabe CK, Wood WI, Zhang Z;
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N-PSDB; AAS46116.
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21-MAR-2000;
28-MAR-2000;
29-MAR-2000;
29-MAR-2000;
30-MAR-2000;
04-APR-2000;
11-APR-2000;
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03-MAY-2000;
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30-MAY-2000;
02-JUN-2000;
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AAB87591 standard: Protein: 649 AA AAB87591;

(first entry) Human PRO1865. Human, PRO protein; mapping Homo sapiens

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susceptibility to tumour development, particularly datean, lung, colon, wases, prostate, rectal, cervical, or liver tumours, in manmelian manjest; prostate, rectal, cervical, or liver tumours, in manmelian pubjects ; Ro oligopucchedide probes specific for the Rob nouled cacide can be used for genetic analysis of individuals with genetic disorders.

WO200116318-A2 38-MAR-2001.

2000MO-US04341. 2000MO-US04342. 2000MO-US04414. 2000MO-US05601. 24-AUG-2000; 2000WO-US23328 99WO-US20111 99US-0169495 903-0170262 2000US-0175481 18-FEB-2000; 18-FEB-2000; 22-FEB-2000; 01-MAR-2000; 01-SEP-1999; 15-SEP-1999; 07-DEC-1999; 09-DEC-1999; 11-JAN-2000; X8X8X8X8X

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100.0%; Score 3400; DB 22; 100.0%; Pred. No. 7.5e-290;

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Best Local Similarity 100. Natches 649; Conservative

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                                                                                                                       AAB70533 standard; Protein; 649 AA.
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molecular biology, including use as hybridization probes, and in
                                                                                 Godowski PJ;
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                                                                  Goddard A,
Wood WI;
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; Pred. No. 7.5e-290;
0; Mismatches 0; 3
                                                                          Gerritsen ME,
Watanabe CK.
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                                                                          Eaton DL, Filvaroff B,
Grimaldi CJ, Gurney AL,
(GETH ) GENENTECH INC
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RESULT 4 ABB95559

ABB95559 standard; Protein; 649 AA ARR95559: 22522

19-JUL-2002 (first entry)

Buman anglogenesis related protein PRO1865 SEQ ID NO: 274.

Buman; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atthered; gene therapy; endotheilal disorder; atthered; antidangiogenic; hypotensive; vulnerary; antiarteriosclerotic.

W0200208284-A2. domo sapiens.

31-JAN-2002.

09-JUL-2001; 2001WO-US21735 2000US-219556P 2000US-220624P 20-JUL-2000;

2000WO-US20710 2000US-222695P 2000US-0643657 2000WO-US23522 2000WO-US23328 2000US-230978P 20000S-000000P 2000US-0664610 200005-0665350 2000US-242922P 2000US-0709238 25-UUL-2000; 25-UUL-2000; 28-UUL-2000; 02-MUG-2000; 17-MUG-2000; 17-MUG-2000; 17-MUG-2000; 17-SEP-2000; 18-SEP-2000; 18-SEP-2000; 18-SEP-2000; 24-OCT-2000; 08-NOV-2000; 08-NOV-2000;

2000WO-US30952 2000WO-US30873 2000WO-US32678 2000US-0747259

01-DEC-2000; 20-DEC-2000;

ö Length 649; Indels DB 23; Query Match 100.0%; Score 3400; DB 23; Best Local Similarity 100.0%; Pred. No. 7.5e-290; Matches 649; Conservative 0; Mismatches 0;

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100.0%; Pred. No. 7.5e-290;
.ive 0; Mismatches 0; Indels 0;
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Godowski EV, Gurney AL, Elliam KJ, Warsters SA, Pan J, I
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
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                      Sest Local Similarity Luc.
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TOSISKIPTLERLHLDDNSVSAVSIREGAPROSNYLRLIPLSRNHLSTIPWGLPRTIREL 180
                                                                            121 YDSLSKIPYLEELHIDDNSVSAVSIEEGSAFRDSNYLRILFLSRNHLSTIPWGLPRFIEEL 180
                                                                                                                                                        RLDDNRISTISSPSIOGLISLKRIVIDGNILLNAHGI, GDKVFFNILVNLTELSLVRNSITAA 240
                                                                                                                                                                                                                                                                                                                PVNIPGTNIAKLYLQDNHINRVPPNAFSYLRQLYRLDMSNNNLSNLPQGIPDDLDNITQL 300
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2000US-222695P
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23-AUG-2000;
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                                                                      PUNLPGTNIERLITLODNHINRVPPNAFSTLROLYRLDMSNNNLSNLPOGIFDDIDNITOL 300
                                                                                 ILRNNPWYCGCKMRWYRDWLQSLPVKVNVRGLMCQAPEKVRGMAIKDLMAELFDCKDSGI 360
                                                                                                                                          ILRNHPWYCGCRMRWYRDWLQSLPVRVNVRGLMCQAPEKVRGMAIKDLMAELFDCRDSGI 360
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121 YDSLSKIPYLEELHLDDNSVSAVSIREGAFRDSNYLRLLFLSRAHLSFIPWGLPRTIEEL 180
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                      181 RIDDNRISTISSPSIOGIJSIKRIVIDGNILINNHGIGDKVPFNLVNIJELSLVRNSLTAA
                                               181 RIDDNRISTISSPSIOGITSLKRLYLDGNILLNNHGLGDKVFFNLVNLFELSLYRNSITÄR
                                                                                                                                                                 VSTIGITTALPNITYPAGGGWPAPVIKQPDIKNPKLIKDQQTIGSPSRKTITITVKSVTS
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A, Nagai K, Otsuki T;
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Sugiyama T, Wakamatsu
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11-JAN-2000; 2000JF-0118776
02-WAY-2000; 2000JF-0183767.
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Claim 8: SEC ID 13435: 2537pp + CD ROW: English.
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the present invention describes primes, rest or synthesis story 550.

All-langth colors defined in the specification, Where a primer set organization of complementary comprises; on a cliptory financial complementary complement of the present invention.

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481 PMETSNIYLEDETPVCIETETAPLRMYNPTTTLNREQEKEPYKNPNLPLAAIIGGAVALV 540

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                                          TTT FLOWNOINNAGIPSDLKNILKVERITIZHNSLDERPTNLPKYVKELHIORNNIRTIT 120
                                                                                                                                                                     YDSLSKIPYLEELHLDDNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEEL 180
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Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
                                                                                                                                                                                                          121 YDSLSKIPYLEELHLDDNSVSAVSIEEGAFRDSNYLKLLFLSKNELSTIPWGLPRTIEEL
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11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
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titsus graveth factor; minumomodalicity; enderco; hasamicpolesis; 
titsus graveth factor; minumomodalicity; enderco; hasamicpolesis; 
nervous system discoder; arthritis; infilamention.
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F, Chen R, Wang 2W;
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601 NEPISKEEFVIHTIPPPNGMALYKNNHSESSSNRSYRDSGIPDSDHSHS 649
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Zhao QA, Wang D, Wang J, Zhang J, Ren F,
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
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                                                                                                                                                         AAM/8907 standard; Protein; 649 AA
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20-70N-2000, 200005-058075-
219-70N-2000, 200008-0654936-
10-588-2000, 200008-0654936-
210-687-2000, 200008-0663851-
30-687-2000, 200008-069382-
30-687-2000, 200008-069382-
                                                                                                                                                                                                                                                                                                                                                       Human protein SEQ ID NO 1569.
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27-APR-2000;
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N-PSDB; AAK94329

Sequence Query Match

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61 TILYLQNNQINNAGIPSDIKNILKVERIYLYHNSLDEFPTWLFKYVKELHLQENNIRTI? 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.9%; Score 3395; DB 22; Length 649; 99.8%; Pred. No. 2.1e-289; Live 0; Mismatches 1; Indels 0.
                                                                                                                                              Claim 8; SEG ID NO 3016; 1380pp + Sequence listing; English.
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AAY76050
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                                                                                                                                                                                                                                                                                                                                               Skip, demail, petilist, derettiooper, monosist, forschist, firbrobland, elemptois skim cell; kerettiooper, stem cell; trensit amplifying cell; secreted transmerbrone; inflamention; concer; menological transmerbrone; inflamention; concer; menological discuss; ansigomentist, stemor vancilarization; growth discoder; deretoperenti discoder; stim vende, inflamention; stim vende, insurpoprotective; valuer;
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that they are secreted. Sequences AAY7986-T5398, AAR7661-T7601,
AAX7616-Y7613-T76121 are proteins with one or more
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Pred. No. 1.2e-279;
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                      181 REDDIKELSTISSPSERGE/SEKREVEDGWILLWHGE/GDKVFPREVE/NEESEVRASEFAA 240
                                                                                                                                                         VSTIDITTAIPMINYPAGGGWPAPVIKOPDIKNPKIJKDOGTIGSPSRKIITIVKSVTS 420
                                                                                                                                                                                                                             DTIHISWKLALPMTALKLSWLKIGHSPARGSITETIVIGERSEVIVTALEPDSPYKUCHV 480
                                                                                                                                                                                                                                                                                           DTHISWRIALPASWIALELSWIKLGHSPARGSITFILVTGERSEYLVTALEPESPYRVCAV 480
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                                                                                                                                                                                                                                                                                                                                                                            PMETSNLYLPDETPVCIETQTAPLRAYNPTTTLAREQEKEPYKNPNLPLAAIIGGAVALV 540
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                                                                                                                                        II.RNNPWYCGCKMKWVRDWI.OSI.PVKVNVRGI.MCOAPEKVRGMA.IKDLNAEL.PDCKDSGI 360
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   RIDDIRISTISSPSIOGLESLKRIVIDGNILINNHGIGDKVFPNLVNILFELSLVRNSILFAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      noctropic, neuroprofective, vulnerary, immunomodulatory, vaccine, keratinocyte growth stimulation; cancer, angiogenesis inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a polypeptide which is expressed in
mammalian skin cells. The polypeptide is useful for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kumble KD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDISKERFVIHTIFPPNGMALYKNMHSESSSMRSTRDSGIPDSDHSHS 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse, skin cell; cytostatic; antiinflammatory; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEDISKEERVIH TEPPNGMILKNNISESSSINSIKOSGIPDSDESS
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28-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kumble KD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wew polymucleotides and polymeptides encoded by the polymucleotides isolated from skin edils, useful for treating skin wounds, cencers, growth and developmental defects, inflammatory diseases, or for modulating immume responses.
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96.5%; Pred. No. 1.2e-279;
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25-JUL-2000; 2000US-221232P.
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Rosen Ch. Barash SC, Ruben SM; (HUMA-) HUMAN GENOME SCI INC.

Nucleic acid molecules encoding human secreted extracellular matrix process, used in preventing, treating or imblicating a disorder, e.g. Alzheimer, and Parkhison's diseases and cancers -

Claim 11; SEQ ID No 276; 577pp; English.

The invention with the to included an include an extending the present of which will not be a polymerical child and provides are wested to present region. The proposes (989). The proposes of arrest, tachycardia and angina), infections caused by bacteria, viruses and fund; and coular discretes (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation.

0; Gaps Length 623; Indels Query Match 96.3%; Score 3274; DB 22; Best Local Similarity 100.0%; Pred. No. 8.5e-279; Matches 623; Conservative 0; Mismatches 0;

Wed Apr 23 13:51:17 2003

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61 RIVLYBNSLOEPPUNLDKYVKELHJOENNIRTIYOSLSKIPYLEELHIDDNSVSAVSIE 120
                                                                                                                                                                                                                                                                      121 EGAFRDSNILELLFLERNHLSTIPWGLPRTIEELRLDDNRISTISSPSIQGLISIKRIVE 180
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ABP47846 standard: Protein: 623 AA RESULT 13

ABP47846;

23-AUG-2002 (first entry)

Human polypeptide SEQ ID NO 276

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Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polymucleotides, particularly the 5602 mill-length contact expection in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RIYLYENSLDEPPINLPKYVKELHIQENNIRTITYDSLSKIPTLEELHIDDNSVSAVSIE 120
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Pred. No. 2.3e-278;
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Otsuki I
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A, Nagai K,
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T. Wakamatsu
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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                              Homo sapiens.
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02-MAY-2000;
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27-AUG-1999;
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Gaps

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Ruman; primer; detection; diagnosis; antisense therapy; gene therapy

Human protein sequence SEQ ID NO:12162.

(first entry)

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ineigh excited onks. Litture that were synthesised by the oligo-cappia
method. The priests making the production of the full length onks assily
without any special methods. The present eceptons is a polymetride encoded by a full length human onks of the invention. Only the work when the sequence data for this patent of all one forms part of the printed specification, but was obtained in On-RMA formst directly from 1800.
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                                                                                                                                                                       Length 627;
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                                                                                                                                                                       Score 3261; .DB 22;
Pred. No. 1.2e-277;
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Job time : 42 secs
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                                                                                                                                                                   tch 95.9%;
al Similarity 99.5%;
623; Conservative
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                                       141 FSYLRQLFRLDMSNINLESNIPQGIFDDLDNITQLILRNNFWTCGCRMKWVRDWLLGSIPVK 300
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                                                                                                                                                                                     361 KQPDIKNPKLFKDHQFTGSPSRKTITITVKSVTSDTHISWKLALPMTALRLSWLKLGHS 420
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                     267 FSYLRQLYRLDMSNNNLSNLPQGIFDDLDNITQLILRNNPWTCGCKMKWVRDWLQSLPVK
                                                                                        VNVRGIACQAPEKVRGMAIKDINAELFDCKDSGIVSTIQITTAIPWIVIPAQGQWPAPVI
                                                                                                                 301 VNVRGIMCOAPBKVRGMAIKDINAELPDCKDSGIVSTIOITTAIPNTVYPAOGOMPAPV
                                                                                                                                                                   387 KOPDIKNPKLIKDOOTIGSPSRKTITITVKSVTSDIIHISWKLALPMTALKLSWLKIGHS
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T, Koga H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              claim 8; SEQ ID NO 3863; 1380pp + sequence listing; English.
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Wakamatsu A, Sugiyama T, Nagai K, Kojima S,
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Total number of hits satisfying chosen parameters: 262574 seqs, 29422922 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and its derived by analysis of the rotal score distribution.

SUMMARIES

Description	Sequence 305, App	Sequence 124, App					Sequence 7, Appli				Sequence 2, Appl1		Sequence 2, Appl1		Sequence 48, Appl	27	ć	rì	Sequence 2, Appli	÷	Seguence 4, Appli	rì	ř	5	'n	43	Sequence 5, Appli
А	US-09-188-930-305	US-09-188-930-124	US-09-131-648-2	US-09-182-024A-2	US-09-063-950-2	US-09-182-024A-5	US-09-191-647-7	US-09-540-245A-7	US-09-540-153-7	PCT-US91-09055-2	US-09-191-647-2	US-09-540-245A-2	US-09-540-153-2	US-08-442-063A-45	US-08-442-0633-48	US-08-442-063A-27	US-08-272-919-2	US-08-619-916-2	PCI-US95-08542-2	US-08-303-238-4	US-08-458-834-4	US-08-303-238-1	US-08-458-834-1	US-08-303-238-2	US-08-458-834-2	US-09-724-864-43	US-08-986-485-5
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Score	3284	546	397	377.5	354.5	345.5	344.5	344.5	344.5	344.5	343.5	343.5	343.5	342	342	342	342	342	342	342	342	335.5	335.5	333.5	333.5	320.5	316.5
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314.5	9.5	605	-	US-08-190-802A-49	Sequence	
314.5	9.5	605	4	US-08-477-346-49	Sequence	49. App
314,5	6	605	4	US-08-473-089-49	Seguence	
314.5	9.5	605	4	US-08-487-072A-49	Sequence	49. App
311.5	9.5	605	4	US-09-063-950-5	Seguence	5. Appl
306	9.0	603	н	US-08-190-802A-50	Seguence	50. App
306	9.0	603	4	US-08-477-346-50	Sequence	50. App
306	9.0	603	4	US-08-473-089-50	Seguence	50, App
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303	6.8	353	φ	5340934-4	Patent No.	534093
299.5	8.8	236	н	US-08-442-0638-42	Seguence	42. App
294	9.0	1101	е	US-08-986-485-2	Seguence	2. Appl
283.5	8.3	368	н	US-08-303-238-3	Sequence	3. Appli
283.5	8.3	368	4	US-08-458-834-3	Sequence	m
277.5	8.2	368	6	5340934-2	Patent No.	٠.
268.5	7.9	224	S	PCT-US91-09055-4	Sequence	-1
260	2.6	231	m	US-08-986-485-7	Seguence	7. Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 DSLAVDNLP--DLRKIEATNNPRLSYIHPNAFFRLPKLESLAGINSNALSALYBGTIESLP 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    413 RDMMRICLPLIAPESFPSNLNVEAGSYVSFHCR----ATAEPQPEIYWITPSGQKILLPN 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409 KTITITVKSVTSDTIHISWKLALPWTALRLSW ---LKLGHSPAFGSITETIVTGERSEYL 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 PEDATILITIONNOI------RRAGIPSDIKNILKVERI------TLYBNS 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 23.28; Fred. No. 4.7e-27;
Matches 173; Conservative 114; Mismatches 240; Indels 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 708;
4.7e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.7%; Score 397;
23.2%; Pred. No. 4.
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Patent No. 6342370
GENERAL INFORMATION:
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Rajput, Bhanu
                                                                                                                                                                                                                                                                                                        JOTHER INFORMATION: 2687731
US-09-131-648-2
                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
SOFTWARE: PERL Program
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                                                                                               ENGTH: 708
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                                          SEO ID NO 2
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                                          361 VSTIQITTAIPNTVYPAOGOWPAPVTKOPDIKNPKLTKDOOTIGSPSRKTITITVKSVTS 420
                                                                                                                                                                                                                                                              480
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                                                                                                                                         361 VSTICITTAIPNTAYPACCOMPAPYTKOPDIKNPKLIKDORTIGSPSRKTILLITVKSVTP 420
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TITLE OF INVENTION and Methods For Their Use
FIRE REFERENCE: 1100-1.01cl G. GREAT APPLICATION NORMER: 08/09/189,930A
GURRENF FILEND NATE: 1999-11-09
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APPLICANT: Octley, Well C.
APPLICANT: Gospler, Karl J.
APPLICANT: Gospler, Karl J.
APPLICANT Gospler, Karl J.
APPLICANT PAPLESON, CHANGESON, CHANGESON, TRIVERGEBORGE, TRIVERGEBORGE, 19-0576
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Pred. No. 8.4e-42;
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Patent No. 6150502
GRNERAL INFORMATION:
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APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  582 SVQEIMITGNQLETVHGRVFRGLSGLKTIMIRSNLISCVSNDTFAGLSSVRL----LSLY 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ISAAWSIFLIGIKIGLFLOVAPLSVM----AKSCPSVCRCDAGFIYCNDRFLISIPTGIP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 377.5; DB 4; Length 1523;
; Pred. No. 9.3e-25;
95; Mismatches 243; Indels 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                491 DE-----PPUCIBTETAPLRMYNPTTTLNREGEKEPYKNPNLPLA 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNRITTITEGAETTLVSPVHHKPPVQPLQLQ-----LPLA 672
                                                              TILE OF INVESTOR: SMALL SERVICES AND STATE OF INVESTOR SHOWS THE STATE OF SMALL SHOWS AND STATE OF SMALL SHOWS AND SMALL SHOW SMALL SHOW AND 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 22.4%;
Matches 158; Conservative 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Ver. 2.1
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 991
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APPLICANT: Connolly, Timothy APPLICANT: Redput, Bhann Prints OF INTERFORT INTERFICANT: Human Slit Polypeptide and Polynucleotides Encoding
                                                                                                                                                                                                                                                                                                           71 -NNAGIPSDLKNILKVERIYLYHNSLDEFPTNLPK---YVKELHLQENNIRTITYDSLSK 126
                                                                                                                                                                                                                                                                                                                                                                                    70 GSFAGLPG-----LQLLDLSQNQIASLPSGVFQPLANISNLDLTANRLHEITNEFFRG 122.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 LRRLERLYLGKNRIR--HIQPGAFDTIDRILEIKLQDNRIRALPPLRIPRI----ILIDLS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 RISTIS-SPSIQGLTSLARLVLDGNILINNEGLGDKVFFNLVNLTELSLVRNSLTAAPVNL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 PG-TNLRKLYLQDN-HINRVPPNAFSTLRQLYRLDMSNNNLSNLPQGIFDDLDNITQLIL 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 RHNPWYCGCKAKKWVRDWLQSLPVKV-NVRGLACQAPEKVRGMAIKDLNAELFDCKDSGIV 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 ARNPENCYCPISWPEGPWVRESHVILASPEETRCHFFPKNAGRLILELDYADFGCPRATTT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 STIQIT-----TAIPNIVIPAGGGWPAPVIKQPDIKWPKLT------397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               356 AIVPTTRPVVREPTALSSEAPT---WLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPS 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 TCLINGSTCHLGTRHHLACLCPEGFTGLYCESQMGGGTRPSPTPVTPRPPRSLTLGIEPVS 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420 SDTIHISWKLALPWIALRLSWLKIGHSPARGSITETIVT----GERSEYLVTALEPDSPY 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       476 KVCMVPMETSNLYLEDETPVCIETETAPLRMIN--PTTTLAREQEKEPYKNPNLPLAAII 533
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                                                                                                                                                         17 LPLQVAPLSVMAKSCPSVCRC-DAGFIYCNDRFLTSIPTGIPEDATTLYLQNNQI---- 70
                                                                                Indels 119;
Owery Match 10.4%; Score 354.5; DB 4; Length 673; Best Local Similarity 24.55; Fred No. 36-23; 36-23; Matches Lös; Conservative 101; Mismatches 261; Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      534 GGAVALVTIALLALV-CWYVHRNGSLFSRNCAYSKGR 569
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; Patent No. 6342370
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US-09-182-024A-5
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                                                                                                                                                                                                                               Ouery Match
10.1%; Score 344.5; DB 3; Length 1480;
Sest Local Similarity 21.0%; Pred. No. 8.46-22;
Matchles 108; Conservative 60; Mismatches 133; Indels 149; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 NLLKVERIYLYHNSLDEFPINLP-----KYVKHLHIOENNIRTIYYDSISKIPYLHEL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333 ------FITELPPKSFSFRRIERIDLSNNNISRIAHDALSGLKOLTTL 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            434 ANGTEDAMKSMKTVHLAKNPFICDCNLRWLADYLHKNPIETSGARCESPKRMHRRRIESL 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      494 REEKFRCSWGELRMKLSGECRMDSDCPAMCHCEGTTVDCTGRRIKEIPRDIPLHTTELLL 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  554 NDNELGRISSDGLFGRLPHIVKLELKRNQLFGIBPNAFFGASHIQREQLGENKIKRISNK 613
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                                                                                                                                                                                                                                                                                                                                                                                                                           22 APLSVMAK-SCPSVCRCDAGFIYCNDRFLTSIPTGIPEDATTLYLQNNQINNAGIPSDLK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 APLSVAGK-SCPSYCRCDAGFIZCNDRFLFSIPTGIPEDATTLYLQHNGINNAGIPSDLK 80
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FILE REFERENCE: B98-031-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ** TATUR WITE STREAM TO NO TO TO TO THE STREAM TO TO THE STREAM THE STREAM TO THE STREAM THE STREAM TO THE STREAM 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326 KVNVRGIMCQAPEKVRGMAIKDLNAELFDC 355
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                                   TYPE: PRT : ORGANISM: Drosophila melanogaster US-09-191-647-7
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APPLICANT: Kid, Thomas
APPLICANT: Katja
APPLICANT: Tessier-Lavigne, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/0
PRIOR FILING DATE: 1998-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2
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TYPE: PRT
        LENGTH: 1480
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US-09-540-245A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285 APMEGGAENSCPHPCRCADGIVDCREKSLTSVPVTLPDDFTDVTLEON----- 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 NILKVERIYLYHNSLDEFFINLP-----KYVKEUHLQENNIRTIYDSLSKIPYLBEL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 HLDDNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIER---LRLDDNRISTI 190
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APPLICANT: Tessica-Lawigno, Marc
TITLE OF INVESTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
                                   FILE REFERENCE: 640100-27.

CORRENT PATLANTON NOBERS: 105/09/182, 024A

CHRRENT FILING DATE: 1999-10-29

PRIOR PETLANTON NOBERS: 60/053,946

PRIOR FILING DATE: 1997-10-31
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EARLIER APPLICATION NUMBER: 60/065,544
EARLIER FILING DATE: 1997-11-14
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BARLIER FLING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATCHIN Ver. 2.0
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1 Sequence 7, Application US/09191647
2 Patent No. 6046015
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                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/C
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 5
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APPLICANT: Kid, Thomas
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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LENGTH: 1480
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48 ADMICOLAROS CTRUCK AND AUTOCORRESTANCE 410 411	OV 114 HLONGYRIV-DIPSOTFRALLALIALISTICATOR STATEMENT 190 376 VLORKIKT-DIPSOTFRALIZATOR 433	OY 191 SESENDALISER. DD 434 ANGTEDAMESMETVPILARINPICCIONLEMALOTLEIGNPLETSGARCESPREMERRETESL 493	Og 203	CQY 212 NORGIGDKYPENLYALIZEGLYANSLIAAPYNLPGYNLACLICDMETHRYPPN 265 DD 554 WDENLAGASSOLGARIA-WILLIAMSCANGOLGERWYRDANSCHORDORDEN 613 DD 554 WDENLAGASSOLGARIA-WILLIAMSCANGOLGERWYRDANSCHORDORDEN 518	Cy 266 APSTLAQLITRILANGRANILGRILANGLYGILDALTQLILRINAPATCOCOGGWYDWIGSLPV 325 Do 614 #FALLIGUTTRINGSCOPPERSPRINGT/SLAGASNPRANCHLANGLAGGER 671	CD 326 KYNYRGIACDAPEKYNGANAIROLARAEPO 355 Db 672 SLAKGGAAROGARSKYNGANAIROLARSER (701	RESULT 9. 12-24-13-17 TO STATE STATE TO THE STATE OF THE), GRRENAL TRYCRACATION: APPLICANT: GOOD OVER TO THOMS APPLICANT: KIG, Thomas	A APPLICANT: Brose, ARANGE, Marc APPLICANT: TREESE-Lavigue, Marc TITED OF INVENTION: TORGULATION ROBO: Ligand Interactions FITTED REFERENCE: 188-101-3	CURRENT APPLICATION NUMBER: US/09/540,153 CURRENT FILTEN DATE: 2000-03-31 PRING APPLICATION NUMBER: 04/10,1547	PROOF FILTMEN DATE: 1998-1-1-13 PROOF FILTMEN DATE: 1998-1-1-13 PROOF FILTMEN DATE: 1998-1-4-07 PROOF FILTMEN DATE: 1998-4-4-07	Supranar Patentin Ver. 2.0 Supranar Patentin Ver. 2.0 Supranar Patentin Ver. 2.0 TYPR: 1940	; ORGANISM: Drosophila melanogaster US-09-540-153-7	Query Match 10.13, Score 344.5; DB 4; Length 1480; Pest Lond Similarity 3.10; Perel No. 84-23; Matches 108; Conservative 60; Mismitches 133; Indels 149; Gaps 10;	CQ 22 APLSVAMA.SCPSUVGACDAGPITCNGSPASIPTGIPEDAFTLYLQNNINNACIPSDLX 80	LSKI	134 HLDDNSVSA	Db 376 VIZGRCIK-DESCVPICIOSIRULALANDRISCIRKONPROLISISICALISITORIN 133 Qy 191 SSENGOLISIK - 202

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                                                                                                                                                                   Query Match

10.1%; Score 343.5; DB 3; Length 1525;
Best Local Similarity 23.9%; Pred, No. 116-21.
Matches 119; Conservative 55; Mismatches 165; Indels 159;
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Apprican; Edd, Thousa
Neptican; Toda, Thousa
Neptican; Toda; Chinasa
TITLE GO HIVERTOR; Mediating Robe: Ligand Interections
TITLE REPRESENTE: 199-037, 940-345.
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23.9%; Pred. No. 1.1e-21;
ive 55; Mismatches 165;
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PRIOR APPLICATION NUMBER: 60/065,544
PRIOR FILING DATE: 1997-11-14
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PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
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Patent No. 6270984
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SOFTWARE: Patentin Ver. 2.0
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Matches 119; Conservative
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APPLICANT: GOODMAN
                                        ; ORGANISM: human
US-09-191-647-2
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ORGANISM: human
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SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 NILKVERIYLZHNSIDEFPINLP-----KYVKELHIQENNIRTIYDSIGKIPYLEEL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 ------FITELPPKSFSFRELRIDLSNNNISRIAHDALSGLKOLTTL 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 VLYGNKIK -- DLPSGVPKGLGSLRLLLLNANEISCIRKDAFRDLHSLSLYDNNIOSL 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 SSPSLOGLTSLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 10.1%; Score 344.5; DB 5; Length 1480; 
Best Local Similarity 24.(4); Pred 18.0; 8.4e=2.2 Indels 149; Gaps Matches 133; Indels 149; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 ANGTEDAMKSMKTVHLAKNPFICDCNERWIADYLHKNPIETSGARCESPKRMHRRRIESL 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              494 REBEFFCSWGELRMKLSGECRMDSDCPAMCHCEGTTVDCTGRRLKEIPRDIPLHTTELLL 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 554 NDWELGRISSDGLFGRLPHLVKLELKRNQLTGIEPNAFEGASHIQELQLGENKIKEISNK 613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 APLSVAAK-SCPSVCRCDAGFIYCNDRFLTSIPTGIPEDATTLYLONNOINNAGIPSDLK 80
                                                                                                                                                                   IDENTIFICATION METHOD: similarity to epidermal growth OTHER INFORMATION: Involvement in receptor-ligand NAME/KEY: Alternative splice segment LOCATION: 1394 to 1404
IDENTIFICATION METHOD: Similarity to tandem EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Brose, Katja
APPLICANT: Tessier-havigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: 988-031-3
                        OTHER INFORMATION: protein-protein interactions NAME/KEY: 7th MSF-11ke repeat LOCATION: 1353 to 1393
                                                                                                                                                                                                                                                                                                                      IDENTIFICATION METHOD: experimental OTHER INFORMATION: developmentally regulated NAME/KEY: COOR-terminal resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONTRIBUTION OF WALKER OF 1799-1791, 647 CONTRIBUTION OF THE WALKER APPLICATION WINGSTON OF THE WALKER APPLIES OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; IDENTIFICATION NETHOD: experimental PCF-US91-09055-2
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: COOH-terminal region
LOCATION: 1405 to 1480
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Patent No. 6046015
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APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
LENGTH: 1525
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US-09-191-647-2
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Db 54 PRNTERLDLAGNNITRITKTDFAGLRHLAVLQIAENKISTIERGAFQDLKELERLRL 110	QY 91. YHNSIAREPTALPRYVKEIHIQENNIKRITYDGISKIPYIKELIADDNSVANSIBE	DO 148 NORTH, LIFE TRAINER AND LIVE TRAINER OF THE STREET	Db 169 GAFFALROLEVITLANNRYTTENAFRHEPETRFFFERHSNNLYCDCHLAWISDWILRER 746 746	229	Qy 166ISYIPWGLPRIBEIRIDDRISYISSPELGUISALKINIDGRUMANEGIGEN 19h 79a PYSTREGIPPE POWER POWE			OY 278 MSNNMLSNLPQIIDDLDNITQLILRNNPWTCGCKKKFWFDWLQSLPVKYAVRGLKCQAP 337		Db 465 RRIANKRIGQIKSKKFRC 482	MESULT 14 DS-08-42-063A-45 ; Sequence 55. Application US/08442063A	j Patent No. 5705609 ; GBNERAL INFORMATILIA BREKI I. ; APPLICANY: RUCSIANYI, BREKI I.	APPLICANT: PIERSCHBACHER, MICHAEL D. APPLICANT: CARDENING, JOSE	APPLICATI: UCLIA, WILLIAM ; PAPLICANT: WILLIAM : ILVENTINE G. INTRACTORY ERACHENTS AND METHODS OF	TITLE OF INVENTION: INBIBITING CELL REGULATORY FACTORS ; NUMBER OF SEQUENCES: 62	CORRESPONDENCE ADDRESS: ADDRESSES: CAMPBELL AND FLORES CORRESPONDENCE AND ADDRESSES	CITY: SAN DIEGO ; STATE: CALIFORNIA	COUNTRY: UNITED STATES 1 F.P. 9912	COMPUTER MEADING TOWN: MEDIUM THE FLOODY disk COMPUTER TOWN COMMONTHY	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25	CURRENT APPLICATION DATA: APPLICATION NUMBER: 15/08/442,063A	CIALLY DATE: LOWAT-1995 CIALLY DATE: 10-MAI-1995 CIALLY DATE: 10-MAI-1995 CIALLY DATE: 10-MAI-1995	ALON APPLICATION DATA: APPLICATION NOBER: 057/865,652	ATTORNEY AGENT INFORMATION: NAME: CAMPBELL, CATHRIN A.		TELEPHONE: 619-535-901	
1 MISAAWSIDITORXIGIBLE OVA DISONA ROCCESCO CONTRA CON	HKGVGNQNIGISLGLYLAILINKVARQACRAGGGGGGGTVDCHGLAIRSVRNX 53	57 PEDATELYLONNOIN	91 YHNSIDEPPINIPKIVKELHIQBNNIKTITUDSILSKIPVIKELHIDBNSKANSIBE 147	LFPELLFLGTAKLFRLDLSENQIQAIPRKAFRGAVDIKNLQLDTRQISCIED	148 GAPR	166	166LSTIPWSLPRTIEBLRLDDNRISTISSPSLQGLFSLKRLVLDGNLLANHGLGDK 219	289 DCRGRGLFEIPTRLFETTETTLEIGUTIKVIPPGAFSPYKKLRRIDLSNNQISELAPD 346	220 VPFHLVHLPELSLYRNSLFAAPVNL-PGT-NLRKLYLQDNHINRYPPRAFSYLRGUNRLD 277 \	278 MSNNMLSNLPOGLEDDLDNITOLLIANBPWFCGCNKRWTGWIGSLEWKWWREIMCDAP 337	907 LITTORNAL LANGUE SPELANAL VIRTURAR RECUCLIBRATION INTERPLETS - CARCITSF 909 338 EXVRGNAL KDINARLEDC 355	465 RRLANKRIGQIKSKKERC 482	UL 13 19-540-152-2	squence 2, Application US/09540153	SHERAL INFORMATION: PRPILIAM: GOODMAN, COREY	kPLICAT: Kid, TROMAS LPLICAT: Brose, Katja PPLICAT: Tessier-Indian. Marc	TITLE OF INVENTION: Modulating Robo: Ligand Interactions TIER REFERENCE: B98-031-3	CORRENT AFFILCATION NUMBER: US/09/340,153 CURRENT FILING DATE: 2000-03-31 SPINO ADDITORYON NUMBER: 04.191	PRIOR FILING DATE: NORMER: 101217017 PRIOR FILING DATE: 60.081.057	PRIOR FILING DATE: 1998-04-07 WUMBER OF SEQ ID NOS: 14	OOFWARE: Patentin Ver. 2.0 20 ID NO 2 Insurem: 1525	ADDRESS TO THE CONTRACT OF THE	09-540-153-2	March . 10.1%; Score 343.5; DB 4; Length 1525; Store 15.0 of 10.1%; Score 343.5; Decal . 10.21; Score 17.0 of 10.0 of	OVAPL-GUNAR SOPSUC BOTA GOVERNMENT AND THE STATE OF TH	1 MRGVGWQMISILGLYLAILAKVAPQACPAQCSCSGSTVDCHGLALRSVPRNI 53	

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86 NAKISKVSPGAFTPLVKLERLYLSKNOLKELPBKAPFTLQELRAHENEITKVRKVTFNGL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 SKIPYLERLHLDONSVSAVSIEBGAPRDSNYLRLLFLSRNHLSTIPWGLPRITERLRLDD 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 NRISTISSPSLOGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNHTELSLVRNSLTAAPVNL 244
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                                                                                                                                                                                                                                                                                                                                                       82 ------LLKVERIYLZHNSLDEFPTNLPKYVKELHLQENNI----RTITYDSL 124
                                                                                                                                                                                                                                            31 CPSVCRCDAGFIZCNDRFT_SIPTGIPEDATTLYLONNOINNA--GIPSDLKN----- 81
                                                                                                                                                                                    85: Indels 58:
                                                                                                                      Query Match 10.1%; Score 342; DB 1; Length 307; Best Local Similarity 31.9%; Pred. No. 1.1a-22; Matches 90; Conservative 49; Mismatches 85; Indels
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241 P--HIRELHLDNNKLTRVPGGLAERKYIQVY---LHNNKIS 277
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Job time : 22 secs
     n TOPOLOGY: linear
NOLECULE TYPE: protein
US-08-442-063A-48
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                                                                                                                                                  Query Match 10.1%; Score 342; DB 1; Length 282; Best Local Similarity 31.9%; Pred. No. 9.7e-23. Metches 99; Conservative 49; Mismatches 85; Indels 3
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COURSENT PAILOLYCON NA.
APPLICATION NOMBR: US/04442,063A
FILMS PRE: 16-84F.1959/442,063A
GLASSIFFORTON: 514
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ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
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REFERENCE/DOCKET NUMBER: P-LA 1454
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APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
ATTORNEY AGENET INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 48, Application US/08442063A
Patent No. 5705609
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: RUGSLAHTI, ERKKI I.
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TELEFAX: 619-535-8949
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LENGTH: 307 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: CALIFORNIA
COUNTRY: UNITED STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SROTENCES.
TYPE: amino acid
TOPOLOGY: linear
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Gapop 10.0 , Gapext 0.5 PLOSTIM62 Scoring table:

Total number of hits satisfying chosen parameters: 301932 seqs, 80129803 residues Searched:

301932

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database :

11. Ositista Applications, JAN, 1991.
12. Ositista Applications, JAN, 1991.
13. Ositista Applications, JAN, 1991.
14. Ositista Applications, JAN, 1991.
15. Ositista Applications, JAN, 1991.
16. Ositista Applications, JAN, 1991.
17. Ositista Applications, JAN, 1991.
18. Ositista Applications, JAN, 1991.
19. Ositista Applications, JAN,

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result bein printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Query Watch Length DB	8	£	Description	
-	3400	100.0	649	6	US-10-063-547-132	Sequence 132, Apr	
7	3400	100.0	679	6	US-10-004-551-6		
m	3400	100.0	649	6	US-10-174-590-384	384	
*	3400	100.0	649	6	US-10-176-758-384	384, 7	
s	3400	100.0	649	6	US-10-063-616-132	132, 7	
40	3400	100.0	649	6	US-10-175-737-384	Sequence 384, Apr	
7	3400	100.0	649	σ	US-10-063-502-132	132,	
00	3400	100.0	649	σ	US-10-173-706-384	384	
6	3400	100.0	649	6	US-10-175-738-384	384,	
10	3400	100.0	649	6	US-10-175-752-384	384,	
11	3400	100.0	649	σ	US-10-176-482-384	384	
12	3400	100.0	649	6	US-10-176-757-384	384,	
13	3400	100.0	649	σ	US-10-176-913-384	384,	
77	3400	100.0	649	σ	US-10-180-552-384	384,	
15	3400	100.0	649	6	US-10-180-557-384	384,	
16	3400	100.0	649	6	US-10-173-700-384	384	
17	3400	100.0	649	6	US-10-174-572-384	384,	
18	3400	100.0	649	6	US-10-174-579-384	Sequence 384, App	
13	3400	100.0	649	6	US-10-174-582-384	Sequence 384, Apr	

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Sequence	Segment		Sednence	Seguence	Sequence	Sednence	Seguence	Seguence	Seguence	Sednence	Sednence	Sequence	Seguence	Seguence	Seguence	Sednence	Seguence	Sednence	Seguence	Sequence	Sednence	Sednence	Seguence	
200 000 000	US-10-175-743-384	US-10-176-488-384	US-10-176-492-384	US-10-176-747-384	US-10-176-750-384	US-10-176-985-384	US-10-176-987-384	US-10-176-991-384	US-10-176-992-384	US-10-176-993-384	US-10-184-658-384	US-10-173-695-384	US-10-173-697-384	US-10-173-705-384	US-10-174-576-384	US-10-174-585-384	US-10-174-586-384	US-10-175-747-384	US-10-176-481-384	US-10-176-485-384	US-10-176-487-384	US-10-176-493-384	-10-176-756-3	
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ALIGNMENTS

ORMATION:	Eaton, Dan L.	APPLICANT: Filvaroff, Ellen	Gerritsen, Mary E.	Goddard, Audrey	Godowski, Paul J.	Grimaldi, Christopher	Gurney Austin L.
GENERAL INFO	APPLICANT:	APPLICANT:	APPLICANT:	APPLICANT:	APPLICANT:	APPLICANT:	APPLICANT:

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME Gurney, Austin L. Watanabe, Colin K. APPLICANT: Wood, William I. APPLICANT:

Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 170 FILE REFERENCE: P3230R1C1 CURRENT APPLICATION NUMBER: US/10/063,547 CURRENT FILING DATE: 2002-05-02

TYPE: PRT CRGANISM: Homo Sapien US-10-063-547-132

LENGIH: 649

Query Match 100.0%; Score 3400; DB 9; Leagth 649; Best Local Similarity 100.0%; Pref. No. 3.3e.*26.1; Matches 649; Conservative 0; Mismatches 0; Indels 0

Gaps ó

61 TTLYLQNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTIT 120 61 TTLYLONO INNAGIPSOLKNILKVERIYLY HASLDEFTVILFKVELHLOBNITETT 120 1 MISAAWSIFLIGTKIGLFLOVAPLSVARKSCPSVCRCDAGFICNDRFLFSIFTGIPEDA 60 1 MISAAWSIFLIGIKIGLELQVAPLSVMAKSCPSVCRCDAGFIYCNDRFLISIPIGIPEDA 60 Q ð 8

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100.0%; Pred. No. 3.3e-261;
ive 0; Mismatches 0;
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Publication No. US20030008352Al
GENERAL INFORMATION:
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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APPLICANT: PRENNINES, EILM
TITLE OF INVENTION: POLINGUEDIDES AND POLIPEPTIDES ENCODED THEREEY
PILE REPRENEE: 15966-559
                                              181 RLDDNRISTISSPSLOGLISLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAA
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100.0%; Pred. No. 3.38-261;
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UNDERSHE FILIDE DAYE: 2011-27-05
FRICE FRICE PRESS. 09/63,949
FRICE FRICE FRICE PRESS. 09/63,949
NUMBER OF SEQ ID NOS: 110
SEG ID NOS: TO NOS: 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.0%;
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13-10-004-551-6

RESILT

LENGTH: 649 TYPE: PRT

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    61 TILYLONNOINNAGIPSDEKNILKVERIYLYHNSLDEPPTNILPKYVKELHIOENNIRTIT 120
                                                                                                             121 YDSLSKIPYLKELHIDDNSVSAVSIEEGAFRDSNYLRILFISRNHISTIPWGLPRTIEEL 180
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NUMBER OF SEQ ID NOS: 170
SEQ ID NO 132
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Best Local Similarity 100.0%; Pred. No. 3.3e-261;
Micches 649; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/063,616
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Publication No. US20030013855A1
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US-10-063-616-132
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That de Inventories Secretains and Theamsterines and Nucleic
THILE OF INVENTOR: ASSESSED AND THEAMSTERINE POLYPHYIDES AND NUCLEIC
THILE OF INVENTOR: ALLES BROODING THE SHAC
CORRESSOR APPLICATION NUMBER: US/A0.716.738
                                                                               RIDDNRISTISSPSIOGLISLKRIVIDGNILNNHGIGDRVFFNLVNIFBISLVRNSLTAA 240
                                                                                                             241 PVNLPGTNLRKLYLODNHINRVPPNAPSYLROLYRLDMSNNNLSNLPOGIFDDLDNITOL 300
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Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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100.0%; Pred. No. 3.3e-261;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 384, Application US/10176758; Publication No. US20030008353Al ; GENERAL INFORMATION:
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin I.
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Smith, Victoria
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Best Local Similarity
Matches 649; Conserv
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                                                                                                                                                                                                                                                               MISAAWSIELIGEKIGLELQVAPLSVWAKSCPSVCRCDAGFIYCNDRFLTSIPFIGIPEDA 60
                  ; Score 3400; DB 9; Length 649;
; Pred. No. 3.3e-261;
0; Nismatches 0; Indels 0.
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NUMBER OF SEQ ID NOS: 170
SEQ ID NO 132
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Publication No. US20030023042A1
GENERAL INFORMATION:
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APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
         Query Match
Best Local Similarity 100.0
Matches 649; Conservative
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Publication No. US20030013153A1
GENERAL INPORMATION:
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Watanabe, Colin K.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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US-10-175-737-384
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        or Palm
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                                                                                                                                                                                                                                                                                                                                            100.0%; Score 3400; DB 9;
100.0%; Pred. No. 3.3e-261;
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        - See File Wrapper
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Publication No. US20030022294A1
GENERAL INFORMATION:
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 649; Conservative
        Prior Application removed
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 384
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                                                                                                                                                                          ; TYPE: PRT
; OKGANISM: Homo Sapien
US-10-173-706-384
                                                                                                                                                                                                                                                                                                                                                    Query Match
Rest Local Similarity
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US-10-175-738-384
                                                                                                                                 LENGTH: 649
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TITLE OF INVENTION: SERENTED AND TRANSHEMBRIANE POLYPEPTIDES AND NUCLETIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILTER ERPERENCE: PASSAGALCY
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                                                                                                                                                                                                                           Gaps
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                                                                                                                                 Length 649;
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                                                                                                                                 Score 3400; DB 9;
Pred. No. 3.3e-261;
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CURRENT FILING DATE: 2002-06-17
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                                                                                                                                 100.0%;
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APPLICANT GOGDER, Andury
APPLICANT GOGOWSKI, Paul J.
NPELICANT GOTOW, AMSTH. L.
APPLICANT BELL James
APPLICANT SMILLY VICTOR A
APPLICANT SMILLY VICTOR A
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                                                                                                                                                                          Best Local Similarity .....
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) ORGANISM: Homo Sapien
US-10-063-502-132
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                                                                                                                                 Query Match
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RESULT 11
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLIPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                                                                                                                                                                                      0; Indels
                                                                                           Prior application removed - See File Wrapper or Palm
KNAMER OF SEQ ID NOS: 612
SEQ ID NO 384
                                                                                                                                                                                                                                              Score 3400; DB 9;
Pred. No. 3.3e-261;
                                                                                                                                                                                                                                                                                  0; Mismatches
                                                      US/10/175,738
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Publication No. US20030022295A1
GENERAL INFORMATION:
                                                      CURRENT APPLICATION NUMBER: US/10
CURRENT FILING DATE: 2002-06-19
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Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                            Best Local Similarity 100.0
                                    FILE REPERBNCE: P3430R1C45
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                                                                                                                                                                                       ; ORGANISM: Homo Sapien
US-10-175-738-384
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Best Local Similarity 100.0%; Pred. No. 3.3e-261;
Matches 649; Conservative 0; Mismatches no
Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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ORGANISM: Homo Sapien
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Best Local Similarity
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US-10-176-482-384

Sequence 384, Application US/10176482 Publication No. US20030022296A1 GENERAL INFORMATION: APPLICANT: Baker, Kevin P.

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JS-10-176-757-384
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THILE OF INVENTION: SECRETED AND TRANSHEMERANE POLYPEPTIDES AND NUCLEUC
THILE OF INVENTION: ACLDS ENCODING THE SAME
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100.0%; Pred. No. 3.3e-261;
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                                                                                                                                                                                                             Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
Desnoyers, Iuc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       649; Conservative
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Matches 649; Conserv
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APPLICANT: DAMS_CARD.
TITLE OF INVENTION: SECRETED AND FRANSHEMBRANE POLYFEFTIDES AND NUCLEIT COURSING PRESENCE. PLANS EXAMO.
TITLE OF INVENTION: ALIES EXCOUND FEE SAMC.
THE RESERVENT. PLANS AND COURSE SAMC.
CORRENY PLANS DAMS: 3,002-06-20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
Sequence 384, Application US/10176757
Publication No. US20030022297A1
GENERAL INFORMATION:
APPLICANT: BARET Kevin P.
APPLICANT: Chen, Jian
                                                                                                                                                         AFFLICANT: Desnoyers, Inc.
AFFLICANT: Goddowski, Faul J.
AFFLICANT: Goddowski, Faul J.
AFFLICANT: Gurey Amstrin L.
AFFLICANT: Ben, James A.
AFFLICANT: Smith, Victoria
AFFLICANT: Smith, Victoria
AFFLICANT: Wishande, Colin K.
AFFLICANT: Wishande, Colin K.
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601 NBPISKEEFVIHTIPPPNCAMLYKNNHSESSSNRSYRDSGIPDSDHSHS 649

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APPLICANT: Shang-Zemin Arrivation of TRANSARMARE POLIPERTIDES AND NUCLEUC TITLE OF INVENTION: SECRETO ENCODING THE SAME
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                                                               541 TIALIANYOWYUHNIGENERANCAYSKORRAXDDYARAGTEKDNSILEIRETSFOMLPIS 600
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                                                                                                                                                                                                                                           601 NEPISKEETVIHTIPPPNGMNLYKNHSESSSNRSYRDSGIPDSDESIS 649
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Publication No. US20030022300A1
GENERAL INFORMATION:
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APELCONY COCCOSEN, Paul J.
APELCONY COCCOSEN, Paul J.
APELCONY Pau, Jamestin L.
APELCONY Pau, Jamestin L.
APELCONY: Nathanab, Colin K.
APELCONY: Nathanab, Colin K.
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; Pred. No. 3.3e-261;
0; Mismatches 0; Indels 0
CURRENT APPLICATION NUMBER: US/10/176,913
CURRENT FILIND DATE: 2002-06-20
Prior Application removed - See file Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                        Sequence 384, Application US/10176913
Publication No. US20030022298A1
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Best Local Similarity 100.0
Matches 649; Conservative
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APPLICANT: BAKET, KEVIN P.
APPLICANT: Chen, Jian
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US-10-176-913-384
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US-10-176-913-384
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                      APPLICANT: Zhang-Zenin.
TILLE OF INVESTION: SERENTE AND TRANSBERGARE POLYPERTIDES AND NUCLEUT TILLE OF INVESTION: ALSOE SECONDES THE SAME PREPERENCE: PA130NCL147
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481 PMETSNLYLFDETPVCIETETAPLRMYNPTTILNREOEKEPYKNPNLPLAAIIGGAVALV 540
                                                                         541 TIALLALVCHYVHRNGSLPSRNCAYSKGRRRKDDYAEAGTKKDNSILEIREISFOMLPIS 600
                                                                                                541 TIALLALVCWYHRNGSLFSRNCATSKGRRRKDDYARAGTKKDNSILEIRETSFOMLPIS 600
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                                                                                                                                                                                        601 NEPISKREFVIHITEPPNGMALYKNWHSESSSWRSTRDSGIPDSDHSHS 649
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k; Pred. No. 3.3e
0; Mismatches
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CURRENT FILING DATE: 2002-06-25
                                                                                                                                                                                                                                                                                     Sequence 364, Application US/10180557
Publication No. US20030022301a1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                 Desnoyers, Inc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pan, James
Smith, Victoria
Watanabe, Colin K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wood, William I.
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US-10-180-557-384
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Best Local Similarity
Matches 649; Conserva
                                                                                                                                                                                                                                                   RESULT 15
US-10-180-557-384
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APPLICANT
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Hartley, D.A.; Walther, E.; Artavanis-Tsakonas, S., 1988
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C;Comment: This protein binds type I collagen.
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A;Cross-references: GDB:119839; OMIM:125255
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A; Residues: 31-33, 'X', 35-50 <ROU>
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Polygopotatia repeat benoingy (RRI)
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A:Reference number: 806280; WID:88133946; PMID:3435485
A:Accession: 906280
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N'Alternate names: dermatan sulfate proteoglycan II; proteoglycan core protein II
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Cibrer 17. Merilyal Sespence_renision 31. Merilya0 steat_change 20-Aug-1399
Carcession: 806280; 83430; 26545; 26935
Ribuy, A.A.; McGullan, C.I.; Fernise, J.D.; Young, M.R.
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                                                                                                                     RiMaico, Y., Suzuki, S.
submitted to the Rasi Data Library, July 1990
Albestription Niciocide sequences of CDRAs encoding mouse PQI and PQII.
                                                                      A; Cross-references: GB: X53929; NID: c53668; PIDN: CAA37876.1; PID: c53669
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;; Pred. No. 1.5e-15;
56; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch
1 Similarity 28.9%;
91; Conservative 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 -LHNNXISAVGQNDF 307
                                                                                                                                                                                                                                                                                                      A; Reference number: S20811
A; Accession: S20812
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A; Residues: 1-360 <DAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-354 <NAI>
           A; Residues: 1-354 <SCH>
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Charter Arthur Manuschur (Gonse moune)
Charter Arthur (Gonse moune)
Arthur (Gonse M. 18 Santak, S.; Batter, B.; Morgen, Jil.; Benchery, A.M.; Sirad
Arthur (Gonse M. 18 Gonse)
Arthur (Gonse mounte Gonse)
Arthur (Gonse mounte Gonse)
Arthur (Gonse M. 18 Santak)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 0-1869-1997 #sequence_revision 04-Sep-1997 *text_change 20-Aug-1999
C;Accession: 147097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 ELPDIDMIGPVCPFRCQCHIRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIKDGDFK 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 TEVERSUFSGMNOMIVIELGINPLKSSGIENGAFOGMEKLSTIFLADINITTIPOGLPPS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 IBELRIDDARISTISSPSLOGITSLKRLVLDGALLANNEGLGDKVFFNLVNLTELSLVRN- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 LTELHEDGHKITKIDASSLKGINNLAKIGISPN------DISAVDNG 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97; Indels 54;
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                                                                      269 P--HLRELHLONGKLTRVPGGLAEHKYIOVYY---LHNNNIS 305
245 PGTNLRKLYLODNHINRVPPN--AFSYLROLYRLDMSNNNLS 284
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30.9%; Pred: No. 8.4e-16;
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Matches
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Wed Apr 23 13:51:21 2003

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PRINCESSES, N. PRACESSES, M. PARENBERG, D. M. Helnegard, D.; Teardalk, D.R.
Ariticis T. 2007-251, 1954 Assistance, D.M.; Helnegard, D.; Teardalk, D.R.
Ariticis Toricanticulo (the small transcriptial protectival property and fit Appendix SSS775; WID-14179695; PMID-16093066;
Appendix SSS775; WID-14179695; PMID-16093066;
Appendix D. SSS775; WID-14179695; PMID-16093066;
Appendix D. SSS775; WID-14179695; PMID-16093066;
Appendix D. SSS775; WID-14179695; PMID-16093066;
Application of the property of the period of the peri
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C.Dates 23-Aug 1995 seequence_revision 03-Oct-1995 #text_change 24-Sep-1999
C.Accesson SS2275; SS7210; SS2752; 541925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 RDCPQECDCPPNFLFAMYCDNRNLKYLPF-VPSRMKTVFFONNOTTSLOEGVFDNATGLL 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 WIALHGWOITSDKVGRKVFSKLRHIRRLYLDHNNLTRWFGPIPRSLRELHIDHNOISRYP 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 NNALEGLENLTALYLQHDEIQEVG---SSMRGLRSLILLDLSTNHLRKVPDGLPSALEQL 249
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263 NGSLA---NTP--HLRELHINNNKLAKVPGGVADHKFIQVVY---LHNNNISAIGSNDFC 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fibromodulin precursor - human
N/Alternate names: 59K collagen-binding matrix protein
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Local Similarity 32.8%; Pred. No. 2.5e-15;
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                                                                                                                                                                             315 PPGINTKRASYSGVSLESNP 334
                                                                                                      287 POGIFDDLDNITQLILRNNP 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 1q32.1-1q32.1
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A; Residues: 1-376 <HI2>
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PRIME AIR IN IN SHORE J. A. IN SHORE CAN. Relse, L. J. 1860. Chem. 265 2063-2066. 1390
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C.Octes: 10-Aug-1995 Sequence, Persylsion 13-Jan.1995 stext. Lhinge 20-Aug-1999
C.Octes: Aug. 1825 16728; 16728; 285517
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Alriches Gobbys Acts 1137, 235-237, 1992

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A)cross-references: BRBL:212298; NID:957549; PIDN:CNA78170.1; PID:957550
Abandi, V.K.; Dreber, K. .
Bur. J. Cell Biol. 59, 314-321, 1992
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                                                                                                                                                                                                                           C;Keywords: collagen binding; extracellular matrix; glycoprotein Fpl:30/Ommah: signal sequence (fragment) Wateling predicted <8IS> Fpl:54/Product: decorin %status predicted <4GIS> Fpl:55/Product: decorin %status predicted <4GIS> Fpl:57/Promah: proteoglycan amino-terminal homology <PAID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.8%; Score 333.5; DB 2; Length 3' 32.5%; Pred. No. 3.4e-15; tive 37; Mismatches 119; Indels
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A.Molecule type: MRNA
A.Residues: Il-354 <RES>
                                                                                         A;Nolecule type: protein
A;Residues: 90-105;190-199;274-281 <0L2>
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Fig. 127/meatin section to the 2-1/morphote maps banding dash.

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2807 J. 201-2001, 201-201, 201-201, A.; Antonseon, A.;
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C.Dates: 2-Jan-1993 %sequence_revision 22-Jan-1993 *text_change 24-Sep-1999
C.Accession: SGS990; SSG942; SGG640
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A;Accession: S58474
N;Alternate names: corneal chondroitin/dermatan sulfate proteoglycan
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A; Residues: 1-375 <OLD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- similariy; contains 1 ribronectin type iii-like domain.
-i- similariy; contains 10 legicine-rich repeats (lar).
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                                 Fibronectin-like domain-containing leucine-rich transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- FUNCTION: May have a function in cell adhesion and/or receptor
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Nammalis; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat; Repeat; Glycoprotein; Signal.
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N-LINKED (GECNAC. . .) (POTENTIAL).
FF2BF5DG3CA13C92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
- TISSUE SPECIFICITY: Expressed in Kidney and brain.
- PIN: N-41Y009/lated.
                                                                                                                                                                                                                                                                                                                                                                      Approximately 1. Section 1. Section 1. Section 1. M.; Section 1. S
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND GYLCOSYLATION.
MEDLINE-20112755; PubMed-10644439;
Leucine-rich repeat transmembrane protein FLRT1 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
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SMART; SM00082; LRR; 1.
SMART; SM00082; LRR; 1.
SMART; SM00013; LRR; 1.
SMART; SM00369; LRR_TYP; 1.
SLOAL.
SLOAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Senomics 62:417-426(1999)
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                                                                                                                                    Homo sapiens (Human)
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15-708-2007 (Rel. 4), Created)
17-107-2007 (Rel. 4), Last sequence update)
15-007-2007 (Rel. 4), Last amnotation update)
15-007-2007 (Rel. 4), Last amnotation update)
17-107-2007 (Rel. 4), Lest amnotation update)
18-107-2007 (Rel. 4), Lest amnotation u 181 RISTIPLBAFKGINSLRRLVLDGNELANGRIADDTFSRLQNLTBLSLVRNSLAAPPINLD 240 246 GTNIRKLYLÖDNHINRVPPNAFSYLRQLYRLDXSNNNLSNLPQGIFDDLDNITQLILRNN 305 241 SAHLOKLYLODNAISHIPYNYLAKARELERILDISHNNITTIPRGLEDDIGNLAQILLINN 300 306 PHYCGCKMKWVRDWIOSIPVKVNVRGIMCOAPRKVRGMAIKDINARIADCKDS----GTV 361 362 STIQITTAIPN-TVTPAQGQWPAPVTKQPDIKNPKLTKDQQTTGSPSRKTITITVKSVTS 420 421 DTIHISWKLALPWTALRLSWLKIGHSPAFGSITETIVTGERSEYLVTALEPDSPYKVCMV 480 421 DSIRITWKATLPASSPRISMIRIGHSPAVGSITETLAQGDKTEYLLFALEPKSTYIICAV 480 481 PMETSNIXIEDETPVCIETETAPLRAYNPTTIAREOEKEPYKNPKLPLAAIIGGAVALV 540 ONNOINNAGIPSDIKNILKVERIYLYANSLDEFPTNIPKYVKELHLORNNIRTITYDSIS 125 126 KIPYLEELHLDDNSVSAVSIEBGAFRDSNYLRLLFLSRNHLSTIPWGLPFTIEBLRLDDN 185 186 RISTISSPSTOGLISEKRLVIDGNILLNNHGIGDKVFFNLVNILFELSIVRNSELAAPVNLP 245 541 TIAL-LALVCHYVHRNGSLFSRNCAYSKGRRRKDDYARAGTKKDNSILEIRETSFOMLPI 599 6 WSIFILGTKIGLFLQVAPLSVARKSCPSVCRCDAGFIXCNDRFLESIPTGIPEDATTIXL 65 6 W-LFICYGLIAFLIEV----IDSTTCPSVCRCDNGFIYCNDRGLISIPADIPDDATTLYL 60 Bukaryota; Metazoa Chordata; Craniata; Vertebrata; Exteleostomi; Mammalia; Butteria; Primates; Catarrhini; Hominidae; Homo. Lacy S.E., Bonnemann C.G., Buzney E.A., Kunkel L.M.; "identification of Fikhl, Fikh?, and Fikh?; a novel family of transembranch abedine-rich repeat proteins."; Genomics E3:417-426(1999). 600 SNEPISKEEFVIHIPPPNGAMILKANNESS-SSNRSYRDSGIPDSDHSHS 649 SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND GYLCOSYLATION. MEDLINE-20112755; PubMed-10644439; 660 AA PRT. MEDLINE-98116655; PubMed-9455477; SEQUENCE FROM N.A. FISSUE-Brain; 07444988888888888888888888888888 Score 1920.5; DB 1; Length 646; Pred. No. 3.7e-121; 56.5%; Query Match Best Local Similarity

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65 LONNOINNAGIPSDLKNLLKVERIYLFHNSLDEFPFULPKTVKELHLQENNIRTITYDSL 124
                                     70 LENNOLNNAGPARLENNOSVETVYLKGNOLDEPPANLPKAVRVLHFORNNIGTISRAAL 129
                                                                                                                                                                                                                                                                  305 NPWY OGCKWKWYEDWIOSL PVKYNYRGIWOOAPEKVROMAIKDIMAELPDCKDSGIVSTI 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 NPWRCDCSIKWVTEWLKYIPSSLNVRGFMCQGPEQVRGMAVRELNANILLSCPTT--TPGL 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 PLFTPAPSTA-----SPTTQPPTLSIPNPSRSYTPPTPTTSKLPTPDWDGRERVTP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 406 PSRKTITITVKSVTSDTIHISWKLALPMTALRLSWLKLGHSPARGSITETIVTGERSETL 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       466 VTALEPDSPYKVCKVPNETSNLYLPDETPVCIETETAPLRNYNPTTIARROEKEPYK-- 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             480 LVNIEPRSTYRICLVPLDAFNYRAVEDT-ICSEATTHASTLNNGSNTASSHEOFTSHSNG 538
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                                                                                                                                                      130 AQLIKLEELHEDDNSISTVGVEDGAFREAISLAKHILSVPVGLPVDLQELRVDE
                                                                                                                                                                                                                                  185 NRISTISSPSLOGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLFAAPVNL
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Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 OITTAIPNTVYPAGGGWPAPVTKQP--DIKNP--KLIKDQOITGS-----
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STRAINSTORMERS TISSUEDANCEA.
"Alternatively spliced version of the portine decorin gene.";
"Alternatively spliced version of the portine decorin gene.";
"Alternatively spliced version of the portine decorin gene.";
"Internatively spliced version of the portine decorin gene.";
"Internatively spliced version of the portine decoring splice of the post of
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Cloning of the portine decorin gene. ",
Suchintted (FER-1999) to the EMEL/GenBank/DDBJ databases.
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Decorin precursor (Bone proteoglycan II) (PG-S2).
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STRAIN-YORKShire;
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30 MAY - 2000 (Rel. 39, Last sequ
15 - JUN - 2002 (Rel. 41, Last anno
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Eukaryota, Metazoa, C
Mammalia, Eutheria, C
NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Whis surse year entry is operities. It is produced through a collisioner to between the Swiss Institute of Enchromatics and the Bodycam fourtiment of Enchromatics and the Bodycam fourtiment on the Bacycam fourtiment matter, where we no restrictions on its use The more profit is matteriated as loop as its content. In no tay entities returned a present in the nor by entities a littens a personnel (see http://www.isb-sib.ch/Annonney, or send an emit to Intensetis-rish.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN
Ishikawa K.-I., Napase T., Nakajiam D., Seki N., Ohira M.,
Miyajiam X., Tamaka M., Arkundi E., Namara M., Ohara O.,
Predefiction of the coding sequences of unidentified human gene. VIII.
The new CSM clones from brain which code for large proteins in
vitto-.UM
                                                                                                                                                                                                                                  -- STREELLIAR LOCATION: Type I membrane protein (Probable).
-- TISSUE SPECIFICITY: Expressed in pancress, skeletal muscle, brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 45.0%; Score 1530; DB 1; Length 660; Best Local Smilarity 45.6%; Pred. No. 5.26-95; Indels 44; Gaps Matches 305; Conservative 123; Mismatches 194; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 SWILI----SLGLYSQVSKI----LACPSVCRCDRNRVYCNERSLTSVPLGIPEGVTVLY 69

    I- FUNCTION: May have a function in cell adhesion and/or receptor

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat; Repeat; Glycoprotein; Signal. POTENTIAL.
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                   -- PTM: N-glycosylated.
-- SIMILARIY: COWRAINS I FIBRONECTIN TYPE III-LIKE DOMAIN.
-- SIMILARIY: COWRAINS 10 IMDCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
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9B15F283B0D5F778 CRC64;
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SYTOPLASMIC (POTENTIAL).
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LRR 8.
LRR 9.
LRR 10.
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InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_Cterm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
                                                                                                                                                      Res. 4:307-313(1997)
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This STRES-FOOT merty is copyright. It is produced through a collaboration between the Sules institute of Bioinformation and the SEG, outsidence the European Louisfournellos and the SEG, outsidence the European Louisfournellos and the SEG, outsidence of 18 and Priority matching a SEG, and S
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162 BITKVRKAVENGLNOMIVVB---LGTNPLKSBGIBNGAFOGMKKLSYIRIADINITTIPO 218
                                                                                                                                                                                                                                            260 TVDMGSLA---TPP--ELRELHLNNKELKVPGGLAEHKYIOVV---LHWNISAVGSN 311
                                                                   172 GLPRTIBELRLDDNRISTISSPSLOGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTBLS 231
                                                                                                                                       219 GLPPSLTELHLDGNKISKVDAASLKGLNNLAKL-----GLG---FR----SIS 259
                                                                                                                                                                                                          23 LVRNSLTAAPVNLPGTNLRKLYLQDNRINRVPPN--AFSYLRQLYRLDMSNNNLSNL--- 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskaryota; Metazoa, Arthropoda; Mandipulata; Pancrustacea; Hexapoda;
Insecta; Pterryota; Metrera; Badopterryota; Diptera; Brachycera;
Muscomorpha; Empidioldea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rothberg J.M., Jacobs J.R., Goodman C.S., Artavanis-Tsakonas S.; Silti: an extracellular protein necessary for decelopment of midline gils and commissural axon pathways contains both EGS and IRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genea Dev. (4:2169-2187(1990).
-I-PRATION HECESSARI POR DEVELOPMENT OF MIDLINE GLIA AND
-I-ROWSTORL AXON PATHANES. SLIT MAY INTERACT WITH EXTRACELUTAR
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15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                 287 ---POGIFDDIDNITOLILRNNP 306
                                                                                                                                                                                                                                                                                                                                                                                                              312 DECEDERATION STATES 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRR Cterm.
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IPR003591; LRR typ.
IPR001791; Laminin G.
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- Supergraph source Extracellular metrix (by similarity).

- Angebaryty Resource; 2 isocoras, a load form (show here)
and a sport form, are produced by alternative splicing.

- Part. The stronder Syposaminopy brom chan can be other
chondrolful states or ceramical sulface depending upon the tissue
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Best Local Similarity 31.0%; Pred. No. 2.2e-16; Mast Local Similarity 31.0%; Pred. No. 2.2e-16; Indels 64; Gaps Matches 103; Indels 64; Gaps
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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SIMILARITY).
Forms a ternary complex with MFAP2 and ELN (By
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BY SIMILARITY.
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InterPro; IPR003591; LRR_typ.
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EMBL; AF140270; AAD33862.1; -.
InterPro; IPR001611; LRR.
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Pram, PRO0560, LRER, T.
SHART, SM00370, LRER, I.
SHART, SM00370, LRER, I.
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GLYOOPCOCHEIN, EXTLEMENT: I.
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- SUBDAT: Bids to type I and "type II collages, to fibromectin and TOP beta. Forms a ternary complex with MFM2 and ELM (By two. SSQPENCE DE 31-50.

BOOGLING-9007357; PubMed-2590159;

BOOGLING-91.7, White Decled-21/couns of human articular cartilage. The properties of demanna mainfake proceedings and alloches. J. 252: 353-327(1959). Danielson K.G., Parzio A., Othen I.R., Conniterro L., Idezo R.V.; Parielson K.G., Parzio A., Othen I.R., Conniterro L., Idezo R.V.; Phe human decorin gene intron-econo organization, discovery of twa literatively spliced score in the 5° unitraislated region, and snapping of the gene to concern the 5° unitraislated region, and denomines 15:146-156(1933). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo. AMEDINB-67017013; PubMed-3484330; Trusias T. Mescaluft E.; Mescaluft E.; Mescaluft E.; Primary structure of an extracellular matrix proteoglypan core protein deduced from Cloned CMN., S. 83:7683-7687[1986]. of origin. Vetter U., Vogel W., Just W., Young M.F., Fisher L.W.; *Human decorin gene: intron-exon junctions and chromosomal SECUENCE FROM N.A. (ISOPORMS A; B; C; D AND E).
CS-SEADO G, Glant T.T.;
"Altornative of the man decorin.";
Submitted (ANR-1995) to the EMEL/Generak/DDBJ databases. Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases SEQUENCE OF 1-70 FROM N.A. NEDLINE-93162642; PubMed-8432526; MEDLINE-93162643; PubMed-8432527; MEDLINE-87250639; PubMed=3597437; Genomics 15:161-168(1993). SECUENCE OF 31-49. SECUENCE PROM N.A. SEQUENCE PROM N.A. SEQUENCE FROM N.A. TCBI TaxID=9606; localization. TISSUE-Liver; LISSUE-Lung;

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Structure and deduced amino acid sequence of the human fibromodulin

Biochim. Biophys. Acta 1174:204-206(1993). SECUENCE PROM N.A.

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Mus musculus (Mouse). PMOD.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. SEQUENCE FROM N.A. MCBI_TaxID-10090;

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and in the periosteum.

DATECOPENTAL STAGE: Highest levels between 5 days and 1 month of age. Thereaffer. The expression of declined to a level of approx. 336 of maximum, and remained constant throughout the rest of the observation period.
-1- PTM: Binds keratan sulfate chains (By similarity).

-i- PTM: Sulfated on tyrosine residue(#) (Probable).
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-i- SIMILARIY: CONVAIRS 12 LEUCHNE-RICH REPENTS (LRR).

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N-LINKED (GLCNAC.
                                                                          376 AA
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                                                                          35T.
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THEFETO: 180010511, LRR.
THEFETO: 18001052; LRR. CAT.
THEFETO: 18001052; LRR. CAT.
THEFETO: 18001052; LRR. CAT.
FFIRM: 18001051; LRR. 9.
SRATE: 5000701; LRR. 1.
SRATE: 5000701; LRR. 1.
                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
                                                                          SPANDARD:
                                                                                                                                                                                                                                                                                                                                                                                     Nattus norvegicus (Rat).
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STRAIN-Sprague-Dawley;
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REGITTE 10
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Miss STRESPORT marty at copyright. It is produced though a collaboration between the Stress factures of inclinations and the Bout contraction to the Boundard Contraction.

The Boundard Contraction and the Stress was not restrict too the state of the Stress which is the Stress was not restrict to the state of the Stress will be supposed to the Stress will contract a locate agreement the supposed to the Stress will contract the Stress will be supposed to the Stre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 LOELRVHENEITKLRKSDFNGLNNVLVIE---LGGNPLKNSGIENGAFOGLKSLSYIRIS 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 RNHLSTIPWGLPRTIEELRLDDNRISTISSPSLQGLTSLKRLVLDGNLLNNHGLGDKVRP 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 NIVNITELSIVENSLT----AAPVNIPGTNIRKITIQDNHINRVPPN--AFSYLRQLTRI 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 FLIGTKIGLFLQVAPLSVMAKSCPSVCRCDAGFIYCNDRFLISIPTGIPEDATTLYLQNN 68
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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BY SIMILARITY.

O-LINKED (GLYCOSANINOGLYCAN) (BY
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18.9%; Pred. No. 1.4e-15;
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                                                                                                                                                                                                                                                                                                                                                10:
(BY SIMILARITY).

**N-LINKED (GLCNAC. . .) (KERATAN SULFATE)

(BY SIMILARITY).

**N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 APPPPERHOCPOSCDOPPNPPTANYCDNRNLKYLPP-VPSRMXYVFONNOIAALOSGVF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 -NNAG------IPSD-----LKNLLKVERIYLYHNSLDEPPTNLPKYVKELHLOE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 DNATGILWIALHGNOITSDKIGRKVFSKLRHLERLYLDHNNLTRAPGPLPRSLRLHLDH 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 NNIRTITYDSLSKIPYLEELHLDDNSVSAVSIEBGAFRDSNYLRLLFLSRNHLSTIPWGL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOISRVPNNALEGLENLTALYLHHNEIQEVG---SSMRGLRSLILLDLSYNHLRRVPDGL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 PRFIERLRIDDNRISTISSPSLQGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 PSALEOLYLEHNNYTTVPDSYFRGSPKILYVRLSHNSLYNNGLATNY-PNSSSLLEIDLS 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 269:28270-28281(1994).
FUNCTION: May affect the rate of fibrils formation.
SISSUMIN: Binds to type I and type II collagen, to fibronectin and TGF-beta. Poins a ternary complex with MERNZ and EMA (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: The attached glycosaminoglycan chain can be either chondroitin sulfate or dermatan sulfate depending upon the tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 RNSL-TAAPVNLPGINTRKLYLQDNHINRVPPNAPSYL-----ROLYRLDMSNNNLS 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 YNOLOKIPPVN---TNLENLFLQGNRINEFSISSPCTVVDVMNFSKLQVLRLDGNEIKRS 358
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  22 APLSVAAKSCPSVCRCDAGF---ITCNDRPLFSIPTGIPEDATTLYLONNOI----- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi,
Mammalia; Bulberia, Rodentia; Sciuroquathi; Murides; Murinne; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDITARS-SIGNICAL PRABACY-SIGNICAL PROBACY-SIGNICAL PROGRAM J.L., SCHOLZER T., SOLITER M.S., STEARED S.P., T., STEARED L.D., LORGO R.W.; "The marite descrite Complete ON Cloning, general corputation, obromonous a stayment, and sexpression during organogenesis and Listone differentiation,";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of origin (By similarity).

THE SMLL LEUGINE-RICH PROTEOGLYCANS (SLRSS) FAMILY. CLASS I SUBPABLIX.
SIMILARY: CONTAINS 12 LEUCINE-RICH REPEARS (LRR).
                                                                                                                                   341 N-LINKED (GLCNAC. . .) (POTENTIAL)
43219 MW; 9C3298675CE3714A CRC64;
                                                                                                                                                                                                                                                                                                                                                        45,
                                                                                                                                                                                                                                                     ; Score 340.5; DB 1; Length 376;
; Pred. No. 1e-15;
36; Mismatches 121; Indels 45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
11-JUNY-2002 (Rel. 41, Last amnotation update)
Beoorin precursor (Bone proteogyyoan II) (FG-82) (FG60).
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Match Y., Suraki S.;
Shamitted (JU-1990) to the EMBL/GenBank/DBH databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Extracellular matrix.
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                                                                                                                                                                                                                                                                                                                                                                                    Babes tautus (BOVIMB)
Babes tautus (BOVIMB)
Mammalia Rutheria Cetarticdactyla; Ruminantia; Peccra; Bovoidea;
Mominala Povinaes, Dos.
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(SIRED) FAMILY. CLASS I SUBSPARILY.
SIMILARITY: CONTAINS 12 LEGGINE-RICH REPEARS (LNR).
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BORGLIRF-8813956; PubMeds-3455485; D. Young M.R.; DDY, A. McGullan C. C., Termine J.D., Young M.R.; Publicatize clothing and sequence analysis of the cDNM for small stoches. J. 245:801-805(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-9912338; PubMed-2914936;
Choi H.U., Johnson T.L., Pal S., Tang L.H., Rosenberg L.C.,
                                                                                                                                                                                                                                        01-MX-1991 (Rel. 18, Created)
01-MX-1991 (Rel. 18, Latt sequence update)
15-JWN-2002 (Rel. 41, Last annotation update)
Decorin precursor (Bone proteoglycan II) (FG-S2).
                                                                                                                                                                                       360 AA.
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J. Biol. Chem. 264:2876-2884(1989).
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277 DMSNNNLSNLPQGIF 291
                          294 -LHNNNISAVGQNDF 307
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InterPro; IPR000372; LRR_Mterm. InterPro; IPR00352; LRR_cut. InterPro; IPR003591; LRR_typ. Pfam; PF00565; LRR; 8. Pfam; PF01462; LRRNT; 1.

SMART; SM00370; LRR; 2.

EMBL; Y00712; CAA58702.1; -. PIR, S06280; S06280. PIR, B31430; B31430. InterPro; IPR001611; LRR.

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42 PPEVPEIEPMGPVCPFRCQCHIRVVQCSDLGLEKVPKDLPPDTALLDLQNNKITEIKDGD 101
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BhAsryota, Mottaco Chordata, Craniata, Vertebrata, Euteleostomi,
Mommalia, Eutheria, Getartiodactyla, Ruminantia; Pecora; Bovoidea,
Boridae, Captinae, Oris.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
7.1284DAJ08755320 CRC64;
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BY SIMILARITY.
O-LINKED (GLYCOSAMINOGLYCAN) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.9%; Score 336, DB 1, Length 360; 28.8%; Pred. No. 1.9e-15;
SWART; SMO0369; LRR_TYP; 2.
Glycoprofein; Extracellular matrix; Proteoglycan; Repeat;
Leuchine-rich repeat; 91gnal.
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15-JUN-2002 (Rel. 41, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Decorin precursor (Bone proteoglycan II) (PG-S2) (PG40).
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LIRR-S 1.

LIRR-T 2.

LIRR-T 2.

LIRR-T 3.

LIRR-T 4.

LIRR-S 3.

LIRR-T 5.

LIRR-T 5.

LIRR-T 5.

LIRR-T 6.

LIRR-T 7.
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This STRES FOUR entry is expected. It is produced those is collideration between the SALES Institute of Bioinformatics and the BELO cuttation. The Bargoon Bioinformatich institute. There are no self-littings on its use, in one profit institute there are no self-littings on its use, in one profit institute and sea asset as a constant at our manner a self-litting self-litting and self-litting and
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-isminarity and type II and type II collages, to fibromectin and
TOP-bets, Forms a termary complex with MEMP2 and KiM (By
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Goturnix coturnix japonica (Japanese quall).

Adarayota, Metazota (Dovariata, Cranitat, Vertebrata; Buteleostomi; Azotosauria, Nves; Neognatine; Galliformes; Phasianines; Azotosauria, Nves; Neognatines; Galliformes;

    -!- PTM: The attached glycosaminoglycan chain can be either
chondroitin sulfate or dermatan sulfate depending upon the tissue

                                           115 NIRTITIOSLSKIPFIERIHLDDNSVSAVSIEBGAFRDSNYIRLLFLSKNHLSTIPWGLP 174
                                                                                                                                                                                                                                                                                                        162 BITKVRKSVRKGLKOMIVVELGINPIKSSGIENGAFOGMKKISYIRIADINITIEOGLP 221
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SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
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(Rel. 41, East sequence update)
(Rel. 41, Last annotation update)
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Interpro 1 PR0001512 ER8.
Interpro 1 PR000352 ER8.
Interpro 1 PR00352 ER8.
Interpro 1 PR00352 ER8.
Fram: PR00360 ER8. 10.
SFAm: PR00360 ER8. 10.
SRAFT: SR00370; ER8. 3.
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                                                                              Incompaying and Table 10641239; MRIADHIELS P.W.; Incompaying MR W.K., 20040 G., Debt. V. Debts 0.18., MRIADHIELS P.W.; SMR W.K., 20040 G., Debt. V. Debts 0.18., MRIADHIELS C. M. Characterization of Secorit mRNN in pregnant introduction of MRN of Secority of MRN of MRN
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Varient the Access of Control Control
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N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
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BY SIMILARITY.
O-LINKED (GLYCOSAMINOGLYCAN) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.9%; Score 336; DB 1; Length 360;
29.1%; Pred. No. 1.9e-15;
                                                                                                                                                                                                                                                                                                        PUNCTION: May affect the rate of fibrils formation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            osanı; sadu369; LRR_TFP; 2.
Glycoprofein; Extracellular matrix; Proteoglycan; Repeat;
Laucine-rich repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0095D0DFDAB88624 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLCNAC
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HULL SAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRR-T 4.
LRR-S 3.
LRR-T 5.
LRR-T 5.
LRR-T 6.
LRR-S 4.
LRR-T 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thearper, TRR05393; LRR_Out.
Interpro, TRR03593; LRR_Upp.
Pfam. PR00560. LRR. 9.
Stant. PR00462; LRR. 9.
SMART; SW00370. LRR. 2.
SMART; SW001370. LRR. 2.
SMART; SW001370. LRR. 2.
SMART; SW001370. LRR. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR.Nterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF125041; AAF00585.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39972 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 29.1%
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 AA:
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                                                    ISSUE-Myometrium;
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White STRESPORT entry is egyptide. It is produced through a collisheration between the SM48s institute of Sindionation and the BME outlation. The Barnopean individual matterial between the SM49s institute on the Name are no restrictions on its way. By mospeoif, institutions as long as its content, is in so way entities sports a litemage presented that the Name of the SM49s and 
                                                                                                                                                                                   similarity).
Subcaturat towarts (By similarity).
- PM: The attached givosaminosiyoan chain can be either chontroitin sulfate or dermatan sulfate depending upon the tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 CPFRCQCHLRVVQCSDLGLERVPRDLPPDFFLLDLQNNKITFEIKSGDFKNLKNLHALILW 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 ------ELKVERIYLYENSIDEPTHLPRYVKELHIQENNI---RTITYDSL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 NNXISKISPAAPAPIKKLERDIISKINTIKRIPENDPKSIQEIRAHENBISKLRKAVFNGI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 SKIPYLEELHLDDNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIFWGLPRILEELRLDD 184
                                                                                                                  to fibronectin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 CPSYCRCDAGFIZCNDRFLTSIPTGIPEDATTLYLORNOIN--NAGIPSDLKN----- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                  of origin (by similarity).

SIMILARITY: BELONGS OF THE SMALL LEGUINE-RICH PROTEOGLYCANS
(SLAPS) FAMILY. CLASS I SUBENHIX.

-- SIMILARITY: CONTAINS 12 LEMCINE-RICH REPROFIS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .09
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                                                                       Similarity).
--- SIBGNIT: Binds to type I and type II collagen, to fibrone TGF-beta. Forms a ternary complex with MFRP2 and ELM (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.8%; Score 334; DB 1; Length 357; 31.4%; Pred. No. 2.6e-15;
Arch. Biochem. Blophys. 296:190-197(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Primary | Provided |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91; Conservative 51; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31B104c7c3CD711D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY STMILARITY.
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LRR-T 3.
LRR-T 4.
LRR-T 5.
LRR-T 5.
LRR-T 6.
LRR-T 7.
LRR-T 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DECORIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR: S24317; S24317.
InterPro; IPR001511; LRR.
InterPro; IPR000372; LRR_Mterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39687 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZMBL; X63797; CAA45318.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S22197. S22197.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 CPPRCOCHLRYVOCSDIGLERVPRDIPPDTTLIDIONNXITEIRDGDFRALKNIHALILV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 SKIPTLEELHLDDNSYSAVSIEEGAPRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 NOVIVLE---LGTNPLKSSGIENGAFOGNKRLSTIRIADINITSIPKGLPPSLTELHLDG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 NRISTISSPSLOGLISLKRIVLDGNILNNHGLGDKVFFNLVNLTELSLVRNSLIBARVNL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 CPSVCRCDAGFIYCNDRFLTSIPTGIPEDATTLYIQNNQINNA--GIPSDLKN----- 81
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"GDN a Clone to chick corneal chondroitin/dermatan sulfate
profesoflycan reveals identify to decorin."
SMART; SMO0013; LRRNT; 1.
SMART; SMO0369; LRR.TTP; 7.
Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
Lewcine-rich repeat; Signal.
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DEC'1992 (Rel. 24, Last sequence update)
11-JUN-2002 (Rel. 41, Last sequence update)
11-JUN-2002 (Rel. 41, Last emboration update)
Gallus gallus (Chicken).
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MEDLINE-92296735; PubMed-1605630;
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GenCoce Vession 5.1.4_p5_4578 Copyright (c) 1983 - 2003 Compagen Ltd.	OM protein - protein search, using sw model Num on: April 23, 2003, 11:03:31 ; Wilhout Homescape 353:178 Million call uphates/sec	Fitle: US-10-004-551-6 Perfect sore: 340 Perfect sore: 1 NISANSIPLICERIGINIOSSSNISTROSGIPOSGES 649	Scoring table: BlosUn62 (apop 10.0 , dapoxt 0.5		Total number of hiss satisfying chosen parameters: 671580 minimum DB seq ideath: 0 0000000000 messimen DB seq ideath: 20000000000	Post-processing: Minimum March Ow Maximum March District State of Summaries	Database : SFPREMEL_21:* 1: Sp_berchea:* 2: Sp_berchea:*	3 5 5 2 100 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	03 03	15 sp. victoria (16) sp. victo	Pred No. is the number of results practiced by those to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		Result No. Score Match Length DB ID Description	99.9 649 4	1944 57.2 372 4 096442 096442 1942.5 56.5 674 4 08977A2 0947A2	717.3 41.1 708 4 093W5 397 11.7 708 4 098W5 394.5 11.6 707 1 1097860	364 11.3 649 4 Q96A85 364 11.3 653 4 Q96BW1 382.5 11.2 1523 11 Q9WVB4	11 086280 11 087135 11 092676 4 075094

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PUNLEGENLERELYLQDNHINKVPPNAFSYLRQLIYRLDMSNNNLSNLPQGIFDDLDNIYQL 300
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                                                                                                                                                                                                                                                                                                           TILILONNOINNAGIDSDLKNILKVERIYLTHNSLDEPPINLPKYVKELHLOSNNIRTIT 120
                                                                                                                                                                                                                                                                                                                                            61 TILLIONNOINNAGIPSDIKKILKVERIYLYHNSIDEPPYKIPKYVELHIONNIKTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                         121 YDSLSKIPYLEELHLDDNSVSAVSIEEGAFRDSNYTRLLFLSRNEHSTIFWGLPRTIEEL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 RLDDNRISTISSPSLQGLTSLXRLVLDGNLLNNHGLGDXVFFNLVNL/TELSLVRNSL78A 240
                                                                                             Gaps
                                                                                                                                                                      1 MISAAWSIFLIGIKIGLFLOVAPLSVWAKSCPSVCRCDAGFIYCNDRFLTSIPTGIPEDA 60
                                                                                                                                                                                                                                  1 MISAAWSIFLIGTKIGLFLOVAPLSVMAKSCPSVCRCDAGFIYCNDRPLISIPIGIPEDA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVNI.PGTNI.RKLYLODNHINRVPPNAFSYLROLYRLDMSNNNI.SNI.POGIFDDI.DNITOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryoʻta; Metazon; Chordata; Craniata; Vertebrata; Butaleostomi;
Mammalla; Buthata; Primetes; Catarrhini; Hominidae; Homo.
NCBL_maxID=6606;
                                                                                                   ö
                          Score 3396; DB 4; Length 649;
Pred. No. 3.1e-242;
1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEPISKEEPVIHTIEPPROMNLYKNHESBSSNRSYRDSGIPDSDHSHS 649
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01-027-2000 (Trredurel. 15, Last sequence update)
01-9GR-2002 (Trredurel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             662 AA
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                                 99.98;
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KIAA1469.
                                                                  Best Local Similarity 99.8
Matches 648; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9P259
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09P25
010 09P25
010 09P27
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01-DEC-2001 (TrEMBLrel. 19, Created

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de SEGUERRE PORR NA.

SERVICARE PORR NA.

MINISTRA T., CORIN, SURVENI K., SURVENI T., SURVAI Y.,

MINISTRA T., CORIN, SURVENI S., SURVENI A., SURVAI Y.,

MINISTRA T., MINISTRA T., SURVENI S., SURVENI A., SURVENI M.,

MINISTRA T., SURVENI T., TANIGA S., MUCHARRA K., CORO T., TANIGANI S.,

MINISTRA T., TANIGA S., MUCHARRA M., TANIGA S., MUCHARRA T., SURVENI T.,

MINISTRA T., MUCHARRA T., MARMIN T., MARGANI T., MARGANI T., MARGANI T.,

MINISTRA T., MARGANI T., MARGANI T., MARGANI T., MARGANI T., MARGANI T.,

MINISTRA T., MARGANI T.
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01.-MSC-2002 (TENBELcel. 19, Last annoration update)
CDN RAP-7002 (TENBELcel. 20, Last annoration update)
CDN RAP-7004 fis, close MT2R9309716, weakly similar to SLIT protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 MSNNNLSNLPQGIFDDLDNITQLILRNNPWYCGCKMKWVRDWLQSLPVKVNVRGLMCQAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 EKVRGMAIKDINABLEPDCKDSGIVSTIQITTAIPNITYTPAQGQWPAPVIKQPDIKNPKLF 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RKVRGMAIKDINARLEDCKDSGIVSTIQITTAIPWTVTPAGGGWPAPVTKQPDIKNPKLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 KDQQTTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRISWLKLGHSPAFGSITETIV 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           458 TGERSEYLVTALEPDSPYKVCMVPMETSNLYLFDBTPVCIETETAPLRMYNPTTTLAREQ 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518 EKEPYKNPNI-PLAATIGGAVALVTTALLALVCWYVHRNGSI-FSRNCATSKGRRRKDDYAR 577
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                    541 KGRRKKDDYARAGTKKDNSILEIRGTSFOMLPISNEPISKEEFVIHTIPPPNGNNLYKNN 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Front and State (Ruman).
Bikaryota, Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi;
Nammalia; Buthoria; Primates; Catarrhiai; Sominidae; Homo.
NSR_TarzD-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 AA; 41614 MW; A45B2E0E729AB69F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96K42;
01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                           627 HSESSSNRSYRDSGIPDSDHSHS 649
                                                                                                                                                                               601 HSESSENBSTRDSGIPDSDESHS 623
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Matches 369; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY:
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                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     De GENCHOUS PROFILE A. SANIANIA K., SANIANIA R., SANIAR 
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01-DEC-2001 (FFEMELRE). 19, Last sequence update)
11-MAR-2002 (FEMELRE). 20, Last ambritation update)
FEMELRE STREET STRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RIYLYHNSEDEFPTMLPKYVKELHEQENNIRFITYDSLSKIPYLEETHEDDNSVSAVSIE 120
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                                                                                                                                                                               Precursor.
Imos spalens (Human).
Enkaryota, Hetarosa Chordata; Craniata; Vartebrata; Enteleostomi;
Entelesis, Primates; Catarrhini; Bominidae; Homo.
NORM_Entro-606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 99.8
Matches 622; Conservative
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481 PMETSNLYLFDETPVCLETERAPLRMTNPTFTLHREQEKEPYKNPNLPLAALIGGAVALV 540
                                  509 TMETSNAYVADETPVCAKAETAD--SYGPITTINOSONAGPM--ASIPIAGIIGGAVALV 564
                                                                                                                                    541 TIAL-LALVOWYVHRNGSL#SRNCAYSKGRRRKDDYARAGTKKDNSILEIRETSFOMLPI 599
                                                                                                                                                                             409 KTITITVKSVTSDTIHISWKLALPMTALKLSWIKLGHSPARGSITETIVTGERSEYLVTA 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               529 LAALIGGAVALVITAL-LALVCHTVHRNGSLFSRNCAYSKGRRRKDDFARAGTKKDNSIL 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILNE-96207227; PubMed-8619474;
Andersson B., Wentland M.A., Ricafrente J.Y., Lin R., Gibbs R.A.;
'A. 'double adaptor' method for improved shotgun library
construction.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "W. "W. "Section of "section" and "section and "section" and "section and "section" and "section and
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                                                                                                                                                                                                                                                                        600 SNEPISKEEFVIHTIFPPNGMALYKNNHSES-SSNRSTRDSGIPDSDHSHS 649
                                                                                                                                                                                                                                                                                                                        625 -NPTRAKEETVVHTIFPSNGSSLCKATHTIGYGFTRGYRDGGIPDIDYSYT 674
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Pred, No. 4.1e-45;
Pred, No. 5.1e-45;
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01-70W-1998 (TERMELLE) 06, Last sequence update)
01-70W-1901 (TERMELLE) 17, Last annotation update)
1907-Defected 25.6 KMs protein (Fragment).
1900 sapiens (Thuan).
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TISSUE-BRAIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 PWFCGCNLAMLEDWVKARAKAVVNVRGLMCQGPEKVRGMAIKDITSEMDECFETGPQGGVA 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 W-LFLCYGLIAFLTEV----IDSTTCPSVCRCDNGFIYCANDRGLTSIPADIPDDATTLTL 88
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                                                                                                                                                                                                                                                                              Enkaryota: Metazoa: Chordata: Craniata: Vertebrata: Enteleostomi:
Mammalia: Entherla: Primates: Catarrhini: Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.5%; Score 1922.5; DB 4; Length 674; 58.7%; Pred. No. 1.9e-133; Live 92; Mismatches 160; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
InterPro; 198003961, PM.III.
InterPro; 198003961, FW.III.
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674 AA: 74087 MW: 38AB53F7243166CC CRC64:
                                                              WARNAZA (TERMILE). 20, Created)
01-MAR-2002 (TERMILE). 20, Created)
01-UNH-2002 (TERMILE). 21, Last sequence update)
01-UNH-2002 (TERMILE). 21, Last annotation update)
Nomo Sapidos (Humin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR003591; LRR_typ.
IPR001211; PhospholipaseA2.
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SMART; SMO0013; LRRNT; 1.
SMART; SMO0014; LRR_TIP; 8.
PROSITE; PSOOIL9; PAZ_ASP; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000483; LRR_Cterm.
IPR000372; LRR_Nterm.
IPR003592; LRR_out.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Přem; PP0146; LRR; 7.
Přem; PP0146; LRRCT; 1.
Přem; PP0146; LRRCT; 1.
PRINTS; PR01019; LEDRICHPP.
SMART; SM00370; LRR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             #CBI TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LISSUE-BRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
SECURNCE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Sim
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359 NIKEISIHSNPIRCDCVIRMNN-----MNKTNIRFMEPDSLFCVDPPEFQGQNVRQVHF 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               468 TLTDKFYVHSEGTLDINGVTPKBGGLYTCIATNIVGADLKSVAIKVDGSPPODNNGS--- 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   409 KTITITVKSVTSDTIHISWKLALPMTALRLSW---LKLGHSPAFGSITBTIVTGERSRYL 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   525 --INIKIRDIOANSVIVSWKASSKILKSSVKWTAPVKTENSHAAOSAR---IPSDVKVYN 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            466 VTALEPDSPIKVCMVPMETSNLYLFDETPVCIETEJPLRMYNPTTTLNEOEKEPYKNP 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    526 NLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFS--RNC----AYSKGRRRKDDIA--- 576
128 PYLERIALDDNSVSAVSIEEGAPRDSNYLRILFISRNHLSTIP----WGLPRTIEELRID 183
                                                                                                                                        184 DNRISTISSPSLQGLTSLKRLVILDGNLLKNHGLGDKVFFNLVNLTELSLVRNSL---- 237
                                                                                                                                                                                                                                                                                        238 -TAAPVHLPGTHLRKLYLQDN-HINRVPPHAFSYLRQLYRLDMSNNNLSNLPQGIFDDLD 295
                                                                                                                                                                                                                                                                                                                                              301 DSLAUDNIP-DLEKIRATNNPRISTHPARAFRIPKIRSININSNALSALTHGTESIA 358
                                                                                                                                                                                                                                                                                                                                                                                                                         296 NITOLITRANDWICGCRMEWVROWIOSLPVKVNVR----GLMCOAPERVRGAGIK----346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  626 TITLMACLGGLLGIIGVICLI-----SCLSPEMNCDGGHSYVRNYLQKPTFALGE 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMELINEAGURAL B., TORNORM M., TARGEL T.:
"CLORING and Aggression of a novel green for a protein with leucine-
"Lich repeats in the developing mouse nervous system.";
FRAIM Res. Rol. Real Res. 36:45-52(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse),
Bukaryota, Metanza, Chordata, Craniata, Vertebrata, Euteleostomi,
Musmalar Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
Migl.Tarafre-1090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAI-1997 (TrEMBLrel. 03, Created)
01-MAI-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
leuchine-Ich repeat protein precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            707 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      577 ----- EAGTKKDNSILEIRET 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          676 LYPPLINEMERGKEKSTS-LKVKAT 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000483; IRR_Cterm.
InterPro; IPR000432; IRR_CKerm.
InterPro; IPR003592; IRR_CNUT.
InterPro; IPR003591; IRR_CYP.
Pfam; IPR0041; fin3; I.R.
Pfam; IPP00041; fig; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR003961; FN_III.
IPR003598; IG_C2.
IPR003006; IG_MHC.
IPR001611; IRR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 PANTOILLCINNIAKIEYSTDFPUNLIGLDISQUNLSSVTNINVKKAPOLLSVTLBENK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 LDEFP-----TALPK-YVK------BLHLORNNIRTITYDSLSKI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 LIGTRIGLELQVAPLSVMAKSCPSVCRC------DAGFIYCNDRFIZSIPTGI 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Wiemann S., submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                     Homo Sapiens (Human).
Enkarycka, Motazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Memmalia: Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hamano S., Inuzuka H., Morohashi A., Ohira M., Makagawara A.;
Filman neuronal leucine-rich regent profeshi-3(RIRF3).*;
Submitted (MAY-201) to the EMEL/GenBank/DDM datchases.
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                                                                                                                                                                                                                                                     Hypothetical 79.4 kDs protein (Neuronal leucine-rich repeat
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PERMIS PROISE LERNY 1.
PERMIS PROISE LERNY 1.
PRINCE, PROOFIS LERNY 1.
PROPERTY 2.
PROOFIS LERNY 1.
PROPERTY 2.
PROOFIS LERNY 1.
PROPERTY 1.
PROPERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEE-1988) to the EMEL/GenBauk/IDEM databases, submitted (FEE-1988) to the EMEL/GenBauk/IDEM databases, submitted (FEE-1988) to the EMEL/GenBauk/IDEM (ACCOSE).

FEEL, ADDROGST, REMAINELLY.

Interpre, INFOGUSEL, RALEATER.

Interpre, INFOGUSEL, RALEATER.
                                                                                                                                        O.-NRR-2001 (TrEMBLE). 16, Created)
01-MRR-2001 (TrEMBLE). 16, Last sequence update)
01-JUN-2002 (TrEMBLE). 21, Last annotation update)
                                                                    708 AA.
                                                                                                                                                                                                                                                                                        protein-3).
DKF2P761K2424 OR NERR-3 OR RG118D07.1.
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Interpro; IPR000372; IRR_Cterm.
Interpro; IPR003592; IRR_out.
Interpro; IPR003591; IRR_typ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 4-708 FROM N.A.
                                                                           PRELIMINARY;
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Pfam; PF00560; LRR; 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-AMYGDALA;
                                                                                                             043377
                                                                                                             09H3W5:
                                                                           09H3W5
RESULT 7
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RESULT 9

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PP00560; LRR, 10.
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Memmalia; Eutheria; Primates; Catarrhini; Hominidae; Romo.
NCBL_gaxip-e606;
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01-WAR-2001 (TrEMBLE). 16, Last sequence update)
01-DEC-2001 (TrEMBLE). 19, Last annotation update)
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SMART; SMO07010; IRR; 6.
SMART; SMO0032; IRRCT; 1.
SMART; SMO0032; IRRRT; 1.
SMART; SMO0039; IRRRT; 1.
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PRELIMINARY:
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Memmalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NYEBL_FARTD=9606;
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 19, Last annotation update)
Brain tumor associated protein NGOL4.
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THORSTON, TREMOTORS 9. 42.

THEOREM 3. PROMOTORS 9. 42.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        509 PITTLAREOEKEPYKAPALPLA------AIIGGAVALVTIALLALVCWY 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                489 VITSLIPQSTRSTEKTFIPVEDINSGIPGIDEVMKTIKITIGCPVALTIMAAVMLVIFT 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       552 VHRNGSLESRNCAYSKGRRRKDDYAEAGTKKDNSILEIRETSFQMLPISNEPISKEEFVI 611
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11.082-2011 (Transleta.1.20; Late amountaino update)
12.0. Mary-2012 (Transleta.1.20; Late amountaino update)
1800 (Sandreta.1.20; Late promisir.20; Mary-20; M
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Best Local Similarity 24.7%; Pred, No. 58-20;
Best Local Similarity 34.7%; Pred, No. 58-20;
Batches 166; Conservative 86; Mismatches 280; Indels 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      These (2010), thoughten seedical University, Grangshou, China. These (2010), thoughten seedical University, Grangshou, China. Beather, A259958 of CATSCALL. The Reference (2010) and the CATSCALL CATSCAL
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SEQUENCE 649 AA; 72313 AW; 9C11C5ABC7E536CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  649 AA.
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Pfam; PP00560; LRR: 8.
Pfam; PP01463; LRRCT; 1.
Pfam; PF01463; LRRUT; 1.
SMART; SMO0013; LRRNT; 1.
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17 LFLQVAPLSVM----AKSCPSVCRCDAGFIYCNDRFLTSIPTGIPEDA------ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 PKYVKELHLQENNIRTITYDSLSKIPYLÆELHLDDNSVSAVSIREGAFR----- 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 IAIGIAIASIISGPPAAACPTKCTCSAASVDCHGIGLRAVPRGIPRNAERLDIDRNNITR 75
                                                                                                                                                                                                                                                                             ttan W., Shou L., Chen J. R., Wu J.Y., Rao Y., Grnitz D.W.;
"The mouse SLIT family: secreted ligands for ROBO expressed in
patterns that suggest a role in morphogenesis and axon guidance.";

Owr. Biol. 212:290-306(1999).
       Chordata, Craniata, Vertebrata, Euteleostomi,
Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 11.2%; Score 382.5; DB 11; Length 1523; BB ster Local Smilarity 22.8%; Perd. Mo. 38-19; Matches 183; Conservative 104; Mismatches 271; Indels 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1523 AA, 167711 MW, F43A3F3E016C4BFC CRC64;
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Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
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PROSITE: PSOLISE; CTUCLJ: UNKNOWL1.
PROSITE: PSOLISE; CTUCLJ: I. NENOWL9.
PROSITE: PSOUCISE: I. NENOWL9.
PROSITE: PSOLISE: DEPLE: UNKNOWL9.
                                                                                                                                                                                                        STRAIN-SWISS WEBSTER/ICR;
MEDLINE-99365246; PubMed-10433822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000152; Asx, hydroxyl.
IPR000359; Cys_knot.
IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPRO01881; EGF_Ca.
IPRO01439; EGF_II.
IPRO02400; GP_CYSKNOT.
IPRO02049; Laminin_GF.
IPRO01791; Laminin_G.
                                                                                                                                                                                                                                                                                                                                                                                                                                       BRE, AP144629; AAD44760.1; -.
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SM00013; LRRNT; 4.
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       Gukaryota; Metazoa;
Gamalia; Eutheria;
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PROSITE; PS01186;
PROSITE; PS01187;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 ELEDCKDSGIVSTIQITTAIPNTVIPAGGOWPAPVTKQPDIKNPKLTKDQQTTGSPSRKT 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 ASPOCSAPTIMDA ----PRDINISEGRARELECRIPPMSSVEWILPNGTVLSHASRH 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 ITITVKSVTSDIIHISWKL------ALPWTALRISWIKIGHSPARGII 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 PRISV--INDGTLNFSHVILSDFGVTTCMVTNVAGNSAKLNVSTAELNFSNYSFFT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           454 ETIVTGERSEYLVTALEPDSPTKVCMVPMETSNLY---LEDETPVCIETETAPLRMTNPT 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                457 VIVETIELS-----PEDITRENTEPUP-TISTGYOPATICSTVLIQUIRVPROVAVPA 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-ILNREGEK--EPYKNPNLPLAAIIGGAVALVTIALLALVCHTVHRNGSLFSRNCAYSK 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       568 GRRRKDDYAEACTKKDNSILEIRE----TSFQMLPISNEPISKEEFVIHTIFPPNGMNL 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    550 IRKRHQQRSTVTAARTVEILQVDEDIPAATSAAATAAPSGVSGEGAVVLPTIHDHININT 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 KNILKVERIYLFHYSLDEFFTULPKYVRELHLQENNIRTITYDSLSKIPYLEELHLDDNS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 VSAVSIEEGAFRDSNYLRLIPLSRNHLSTIPWGLPRTIEELR---LDDNRISTISSPSLQ 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 GLTSLKRLVLDGNLLNNHGLGDKVPFNLVHLTELSLVRNSLTAAPVNL------ 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 RVPSIAMRIDI-GELKKLEYISEGAFEGIFNIKYINIGMCNIKDMP-NITPLVGLEELEMS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 -----PG----TNLRKLYLQDNHINRVPPNAFSYLRQLYRLDMSNNNLSNLPQGIF 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292 DDLDNITQLILRNNPWFCGCKMKWVRDWLQS-LPVKVNVRGLMCQAPEKVRGMAIKDLNA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 APLSVAGKSCPSVCRCDAGF -- IYCNDRFLFSIPTGIPEDATTLYLONNOINNAGIPSDL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 AAASAGPQNCPSVCSCSNQFSKVVCTRRGLSEVPQGIPSN----- 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 GNHEPEIRPGSFHGLSSLAKLMVNNSQVSLIERNAFDGLASLVELALAHRNLSSLPHDLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 167; Conservative 93; Mismatches 271; Indels 146;
                                                                                                                                                                                                                                                                                                                                                                                                        11.3%; Score 384; DB 4; Length 653; 24.7%; Pred. No. 6.8e-20;
                                      SAMET SHOULDS, TO LIKE 1.
SAMET SHOOLDS, TELLIKE 1.
SAMET SHOOLDS, LEMET, 1.
SAMET SHOOLDS, LEMET, 1.
SAMET, SHOOLDS, LEMET, 1.
SAMET, SHOOLDS, LEMET, 1.
TREMPORTALL LEME, TET, 7.
TREMPORTALL LEME, TET, 7.
SERVERKE, 653 AAA, 72717, MB, 38159021F6850ES7 ORGC4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1523 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLE1, 12,
01-NOV-1999 (TrEMBLE1, 12,
01-DEC-2001 (TrEMBLE1, 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         623 YKNNHSESSSNRSYRDS 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       610 YEPAHGAHWTENSLGNS 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
SM00409;
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152 DSNYLRLLFLSRNH-----

SLIT3 (Fragment). SLIT3. Mus musculus (Mouse).

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Nakamachi K., Matsuoka Y., Kitanaka C., Kuchino Y., Tsuda H.;
Rat neuronal leucine-rich repeat protein-3: cloning and regulation of
                                                  257 NHINRVPP------NAPSYLROLYRLDMSNNNLSNLPQGIFDDLDN 296
                                                                                                                                     227 NHFPEIRPGSFEGLSSLKKLAVMNSHERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRY 286
                                                                                                                                                                                                                                                                   356 KDSGIVSTIQITTAIPNTVYPAQGQMPAPVTKQPDIKNPKLTKDQQTTGSPSRKTITITV 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 SAPFINDA-----PROLNISRDRMAELKCRTPPMSSVKHILDNGTVLSHASRHPRISV 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               416 KSVISDIHISWKLAL-------PMIALRISWLKIGHSPARGSITE-IIV 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 458 TGERS-EYLVTALEPDSPYKVCAVPMETSNIYLFDETPVCIETETAPLRATNPTT-TLNR 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        456 THE STREAM S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             516 BOEK--EPYKAPNI-PIAALIGGAVALVITALIALVCWYVHRNGSI-FSRNCAYSKGRRRKD 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        510 MOTSLDEVMKTTKI ----ILGCEVAVILLABAMLIVEY -----KLRKRHO 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    574 DYARAGTEKDNSILETREISFOMLP-----ISNBPISKEEFVIHTIFPPNGMNLZK 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551 QRSTVTAARTVEIIQVDEDIPAAAPAAATAAPSGVSGE----GAVVLPTHDHINYNYK 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Métazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinse; Rattus.
NCBL_garkD-0116;
                                                                                                                                                                                                                         297 ITQLILRNNPWYCGCKAKKWVRDWLQS-LPVKVNVRGLACQAPEKVRGMAIKDLMAELFDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLEd. 16, Created)
01-MAR-2001 (TrEMBLEd. 16, Last sequence update)
101-UNW-2002 (TrEMBLED. 12, Last annotation update)
Neuronal leucine-rich repeat protein-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lhb gone expression.'
Elicohem. Biophys. Res. Commun. 287:257-263(2001).
Emsin, AF91477 Aacolo644.1;
ThrerPro FR003961; FR_III.
InterPro FR003961; FR_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       707 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SPRAGUE-DAWLEY;
MEDLINE-21433505; PubMed-11549284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; PR000483; IRR_Sterm.
Interpro; PR000372; IRR_Mterm.
Interpro; IPR003592; IRR_out.
Interpro; IPR003591; IRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_KBC.
InterPro; IPR01611; IRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PP00041; fn3; 1.

Pfam; PP00047; 12; 1.

Pfam; PP00560; LRR; 9.

Pfam; PP01452; LRRYC; 1.

Pfam; PP01452; LRRYC; 1.

PRINKS; PR00019; LEURICHEPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           625 NNHSESSENRSTRDS 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      607 PAHGAHWTENSLGNS 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MART: SM00060: FN3: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9XSE60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 KNILKVERIYLYHNSLDEFPTNLPKYVKELHIQENNIRTITYDSLSKIPYLEELHLDDNS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 ----TRYLNIARNNIQMIQADTFRHLHHLEVIQLGRNS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 VSAVSIEEGAPPDSNYLRLLPLSRNHLSTIPWGLPRTIEELR---LDDDNRISTISSPSLQ 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 IR--QIEVGAFNGLASIATLELFDNWL/TVIPSGAFETLSKLREIWLRNNPIESIPSTAFN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 GLISLKRIVLDGNLLNNHGLGDKVPFNLVNLTELSLVRNSLTAAPVNLPGTNLRKLYLQD 256
592 OLETHHORNERGISCHELGGINTLAGE---SQUANDIFAGISSVALLSIIDMRIT 642
                                                                                                                                                                                                                                                                                                                                                      685 SGNPROCKPFFIKEIPIQDVALQDFTCBGNEENSCOLSPRCPBQCTCVETVVRCSNRGLH 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91; Mismatches 274; Indels 146; Gaps
                                                                                                                             512 TINREOEKBPYKNPNIPLAAIIGGAVALVTIALIALV-----CWYVERNGSLESRNCA 564
                                                                                                                                                                                                                         643 TISP-----GAFTTLVSLSTINLLSNPRNCHMANIGRALRERRIV 684
                                                                                                                                                                                                                                                                                                    565 YSKGRRRKDDYARAGTKKDNSILEI-----RRISPOMLPISNEPISKEEFVI-----H 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 AAASAGPONCPSVCSCSNQFSKVVCTRRGLSEVPQGIPSN------75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 APLSVMAKSCPSVCRCDAGF--IYCNDRFLTSIPTGIPEDATTLYLONNQINNAGIPSDL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
Bakaryota Metaroa Choxdeta; Cranieta; Vertebreta; Buteleostomi
Bamania; Butherla; Rodentia; Solurognethi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.1%; Score 378; DB 11; Length 648; 24.3%; Pred. No. 1.9e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nemny J., Bhi L., Id G.,
Nemny J., Bhi L., Id G.,
Salmaitre-specific seems, dwarrequiated in brain tumor.";
Salmaitred (ADG-2000) to the EMEL/GenBank/DDBJ databases.
Interpro; PRO03599; IG.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRARY; SHOROR3; LERCT; 1.
SRARY; SHOROR3; LERCT; 1.
SRARY; SHOROR3; LERCT; 1.
SRARY; SHOROR3; LERCT; 1.
SRARY; SHORORS; LERC_TYP; 6.
SRARY; SHORORS; CRC_G4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TIEMBLEAL 20, Created)
01-MAR-2002 (TIEMBLEAL 20, Last sequence update)
01-UNY-2002 (TIEMBLEAL 21, Last annotation update)
Brain tumor-associated protein MBAGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               648 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003598; IG_C2.
InterPro; IPR001611; IRR.
InterPro; IPR000483; IRR_Cterm.
InterPro; IPR000372; IRR_Mterm.
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InterPro; IPR003591; LRR_typ.
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Pfam; PF01463; IRRCT; 1.
Pfam; PF01462; IRRNT; 1.
PRINTS; PR00019; LEURICHRFT.
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SMART; SM00408; IGc2; 1.
SMART; SM00370; LRR; 5.
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